U.S. DEPARTMENT OF COMMERCE
Patent and Trademark Office

# SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____

Date: _____ Phone: _____ Art Unit: _____

**Search Topic:**

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

## STAFF USE ONLY

Date completed: 03-14-03
Searcher: Beverly Gregg
Terminal time: 20
Elapsed time: _____
CPU time: _____
Total time: 25
Number of Searches: _____
Number of Databases: 1

**Search Site**

_____ STIC
_____ CM-1
_____ Pre-S

**Type of Search**

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

**Vendors**

_____ IG Suite
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
✓ Other CGN

Jiang, D.
10/036,041
seq. IDs 1 & 2 N-Geneseq

GenCore version 5.1.4_p5_4578


OM nucleic - nucleic search, using sw model

Run on: March 13, 2003, 14:39:14 ; Search time 417 Seconds
(without alignments)
9245.614 Million cell updates/sec

Title: US-10-036-041-1
Perfect score: 1712
Sequence: 1 ggcatctgcccgaggagacc.....ttgttaaagataaaaaaaaa 1712

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| | 1 | 1710.4 | 99.9 | 1712 | 21 | AAA96336 | cDNA encoding a no |
| | 2 | 1710.4 | 99.9 | 1760 | 21 | AAA95787 | Human immune syste |
| | 3 | 1696 | 99.1 | 1696 | 21 | AAC64058 | Human zacrp3 cDNA, |
| | 4 | 1695.4 | 99.0 | 1709 | 22 | AAF93874 | Human cDNA encodin |
| | 5 | 1549.6 | 90.5 | 1620 | 22 | AAI99523 | Human polynucleoti |
| | 6 | 1548.6 | 90.5 | 1792 | 22 | AAI59230 | Human polynucleoti |
| | 7 | 1527 | 89.2 | 1927 | 22 | AAD12584 | Human protein havi |
| | 8 | 1363.2 | 79.6 | 1608 | 24 | ABK35221 | Human cDNA encodin |
| c | 9 | 1295.4 | 75.7 | 1799 | 22 | AAI61016 | Human polynucleoti |
| | 10 | 766.6 | 44.8 | 810 | 22 | AAF94076 | Primer specific fo |
| | 11 | 741 | 43.3 | 741 | 24 | ABK35591 | Gene encoding nove |
| | 12 | 696.2 | 40.7 | 1035 | 22 | AAC99776 | Skin cell cDNA, SE |
| | 13 | 696.2 | 40.7 | 1035 | 24 | ABL34928 | Rat cDNA isolated |
| | 14 | 696.2 | 40.7 | 1123 | 21 | AAZ61633 | cDNA encoding rat |
| | 15 | 696.2 | 40.7 | 1123 | 21 | AAZ61730 | cDNA encoding rat |
| | 16 | 696.2 | 40.7 | 1123 | 22 | AAC99566 | Skin cell cDNA, SE |
| | 17 | 696.2 | 40.7 | 1123 | 22 | AAC99663 | Skin cell cDNA, SE |
| | 18 | 696.2 | 40.7 | 1123 | 24 | ABL34718 | Rat cDNA isolated |
| | 19 | 696.2 | 40.7 | 1123 | 24 | ABL34815 | Rat cDNA isolated |
| | 20 | 695.8 | 40.6 | 1117 | 21 | AAC64064 | Mouse zacrp2 DNA, |
| | 21 | 659 | 38.5 | 960 | 24 | ABK35590 | Gene encoding nove |
| | 22 | 544.2 | 31.8 | 738 | 21 | AAC64063 | Human zacrp3 degen |
| c | 23 | 498.6 | 29.1 | 552 | 22 | AAF94215 | Primer specific fo |
| | 24 | 452 | 26.4 | 471 | 21 | AAC02874 | Human secreted pro |
| | 25 | 452 | 26.4 | 472 | 20 | AAX39551 | Human secreted pro |
| | 26 | 345.6 | 20.2 | 472 | 23 | ABV56781 | Human prostate exp |
| | 27 | 208 | 12.1 | 546 | 22 | AAF93419 | cDNA encoding SRT |
| | 28 | 136.2 | 8.0 | 548 | 22 | ABA60188 | Human foetal liver |
| | 29 | 136.2 | 8.0 | 548 | 22 | AAK08465 | Human brain expres |
| | 30 | 136.2 | 8.0 | 548 | 22 | AAK34347 | Human bone marrow |
| | 31 | 136.2 | 8.0 | 548 | 22 | AAI40069 | Probe #8755 used t |
| | 32 | 136.2 | 8.0 | 548 | 24 | ABS09051 | Human genome-deriv |
| | 33 | 130 | 7.6 | 130 | 22 | ABA72727 | Human foetal liver |
| | 34 | 130 | 7.6 | 130 | 22 | AAK21157 | Human brain expres |
| | 35 | 130 | 7.6 | 130 | 22 | AAK47313 | Human bone marrow |
| | 36 | 130 | 7.6 | 130 | 22 | AAI53148 | Probe #21834 used |
| | 37 | 130 | 7.6 | 130 | 24 | ABS21483 | Human genome-deriv |
| | 38 | 121.2 | 7.1 | 900 | 22 | AAF45100 | Human secreted pro |
| | 39 | 80.8 | 4.7 | 909 | 22 | AAC89872 | Human zacrp7 degen |
| | 40 | 78.8 | 4.6 | 435 | 24 | ABL38127 | Human colon tumour |
| c | 41 | 78.8 | 4.6 | 1280 | 22 | AAI99525 | Human polynucleoti |
| | 42 | 78.8 | 4.6 | 2257 | 24 | AAL44063 | Human genset metab |
| | 43 | 78.8 | 4.6 | 2727 | 22 | AAD16945 | Novel human protei |
| | 44 | 78.8 | 4.6 | 2730 | 22 | AAD16951 | Novel human protei |
| | 45 | 78.8 | 4.6 | 2874 | 22 | AAD16947 | Novel human protei |

ALIGNMENTS

RESULT 1
AAA96336
ID AAA96336 standard; cDNA; 1712 BP.
XX
AC AAA96336;
XX
DT 08-FEB-2001 (first entry)
XX
DE cDNA encoding a novel polypeptide designated PRO1484.
XX
KW Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122;
KW PRO1889; PRO1890; PRO1887; PRO1785; PRO4353; PRO4357; PRO4405; PRO4356;
KW PRO4352; PRO4380; PRO4354; PRO4408; PRO5737; PRO4425; PRO5990; PRO6030;
KW PRO4424; PRO4422; PRO4430; PRO4499; tumour; obesity; diabetes;
KW insulinemia; kidney disorder; Bergers disease; nephropathy;
KW Schonlein-Henoch purpura; celiac disease; dermatitis herpetiformis;
KW Crohns disease; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 77..817
FT /*tag= a
FT sig_peptide 77..142
FT /*tag= b
XX
PN WO200056889-A2.
XX
PD 28-SEP-2000.
XX
PF 01-MAR-2000; 2000WO-US05601.
XX

PR 23-MAR-1999; 99US-0125774.
PR 23-MAR-1999; 99US-0125778.
PR 24-MAR-1999; 99US-0125826.
PR 31-MAR-1999; 99US-0127035.
PR 05-APR-1999; 99US-0127706.
PR 21-APR-1999; 99US-0130359.
PR 27-APR-1999; 99US-0131270.
PR 27-APR-1999; 99US-0131272.
PR 27-APR-1999; 99US-0131291.
PR 04-MAY-1999; 99US-0132371.
PR 04-MAY-1999; 99US-0132379.
PR 04-MAY-1999; 99US-0132383.
PR 25-MAY-1999; 99US-0135750.
PR 08-JUN-1999; 99US-0138166.
PR 20-JUL-1999; 99US-0144791.
PR 03-AUG-1999; 99US-0146970.
PR 09-DEC-1999; 99US-0170262.
XX
PA (GETH ) GENENTECH INC.
XX
PI Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2000-628263/60.
DR P-PSDB; AAB18909.
XX
PT Novel secreted and transmembrane polypeptides useful for diagnosing
PT tumour in a mammal, for identifying agonists and antagonists of the
PT polypeptide and for therapeutic use
XX
PS Claim 2; Fig 1; 222pp; English.
XX
CC The present sequence encodes a secreted or transmembrane polypeptide.
CC The specification describes polypeptides designated PRO1484, PRO4334,
CC PRO1122, PRO1889, PRO1890, PRO1887, PRO1785, PRO4353, PRO4357, PRO4405,
CC PRO4356, PRO4352, PRO4380, PRO4354, PRO4408, PRO5737, PRO4425, PRO5990,
CC PRO6030, PRO4424, PRO4422, PRO4430 and PRO4499. PRO1889 polypeptide is
CC useful for diagnosing tumour in a mammal. The polypeptides, their
CC agonists and antagonists are useful treating a condition associated with
CC expression or activity of the polypeptide. Conditions treated include
CC obesity, diabetes or hyper-or hypo-insulinemia. The polypeptides are
CC capable of inducing proliferation of mammalian kidney mesangial cells
CC and are therefore useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Bergers disease or other
CC nephropathies associated with Schonlein-Henoch purpura, celiac disease,
CC dermatitis herpetiformis or Crohns disease. The nucleic acids may be used
CC to generate transgenic animals for use in development and screening of
CC therapeutically useful reagents and also for chromosome identification
CC and tissue typing.
XX
SQ Sequence 1712 BP; 491 A; 358 C; 388 G; 475 T; 0 other;

Query Match 99.9%; Score 1710.4; DB 21; Length 1712;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1711; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1 GGCATCTGCCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GGCATCTGCCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGA 60

Qy      61 GGCTCTGTTGAGAATCATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GGCTCTGTTGAGAATCATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTT 120

Qy     121 TTTCCTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACT 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TTTCCTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACT 180

Qy     181 ACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCC 240

Qy     241 CCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGG 300

Qy     301 AGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCG 360

Qy     361 AGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 AGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGA 420

Qy     421 ACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGAT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 ACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGAT 480

Qy     481 TATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATT 540

Qy     541 TGGGGCCCCAGTATCAGGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGT 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 TGGGGCCCCAGTATCAGGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGT 600

Qy     601 TGAGGAAGTGTATGTGTACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTA 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TGAGGAAGTGTATGTGTACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTA 660

Qy     661 TGAAATGAAGGGCAAATCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TGAAATGAAGGGCAAATCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGG 720

Qy     721 GGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTCCATGGGGACCACCAACGCTTCTC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTCCATGGGGACCACCAACGCTTCTC 780

Qy     781 CACCTTTGCAGGATTCCTGCTCTTTGAAACTAAGTAAATATATGACTAGAATAGCTCCAC 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 CACCTTTGCAGGATTCCTGCTCTTTGAAACTAAGTAAATATATGACTAGAATAGCTCCAC 840

Qy     841 TTTGGGGAAGACTTGTAGCTGAGCTGATTTGTTACGATCTGAGGAACATTAAAGTTGAGG 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TTTGGGGAAGACTTGTAGCTGAGCTGATTTGTTACGATCTGAGGAACATTAAAGTTGAGG 900

Qy     901 GTTTTACATTGCTGTATTCAAAAAATTATTGGTTGCAATGTTGTTCACGCTACAGGTACA 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GTTTTACATTGCTGTATTCAAAAAATTATTGGTTGCAATGTTGTTCACGCTACAGGTACA 960

Qy     961 CCAATAATGTTGGACAATTCAGGGGCTCAGAAGAATCAACCACAAAATAGTCTTCTCAGA 1020
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 CCAATAATGTTGCACAATTCAGGGGCTCAGAAGAATCAACCACAAAATAGTCTTCTCAGA 1020

Qy    1021 TGACCTTGACTAATATACTCAGCATCTTTATCACTCTTTCCTTGGCACCTAAAAGATAAT 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 TGACCTTGACTAATATACTCAGCATCTTTATCACTCTTTCCTTGGCACCTAAAAGATAAT 1080

Qy    1081 TCTCCTCTGACGCAGGTTGGAAATATTTTTTTCTATCACAGAAGTCATTTGCAAAGAATT 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 TCTCCTCTGACGCAGGTTGGAAATATTTTTTTCTATCACAGAAGTCATTTGCAAAGAATT 1140

Qy    1141 TTGACTACTCTGCTTTTAATTTAATACCAGTTTTCAGGAACCCCTGAAGTTTTAAGTTCA 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 TTGACTACTCTGCTTTTAATTTAATACCAGTTTTCAGGAACCCCTGAAGTTTTAAGTTCA 1200

Qy    1201 TTATTCTTTATAACATTTGAGAGAATCGGATGTAGTGATATGACAGGGCTGGGGCAAGAA 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 TTATTCTTTATAACATTTGAGAGAATCGGATGTAGTGATATGACAGGGCTGGGGCAAGAA 1260

Qy    1261 CAGGGGCACTAGCTGCCTTATTAGCTAATTTAGTGCCCTCCGTGTTCAGCTTAGCCTTTG 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 CAGGGGCACTAGCTGCCTTATTAGCTAATTTAGTGCCCTCCGTGTTCAGCTTAGCCTTTG 1320

Qy    1321 ACCCTTTCCTTTTGATCCACAAAATACATTAAAACTCTGAATTCACATACAATGCTATTT 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    1321 ACCCTTTCCTTTTGATCCACAAAATACATTAAAACTCTGAATTCACATACAATGCTATTT 1380

Qy    1381 TAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACCAGTAATGTGGTTGTAATTTTGTGT 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 TAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACCAGTAATGTGGTTGTAATTTTGTGT 1440

Qy    1441 ATGTTCCCCCACATCGCCCCCAACTTCGGATGTGGGGTCAGGAGGTTGAGGTTCACTATT 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 ATGTTCCCCCACATCGCCCCCAACTTCGGATGTGGGGTCAGGAGGTTGAGGTTCACTATT 1500

Qy    1501 AACAAATGTCATAAATATCTCATAGAGGTACAGTGCCAATAGATATTCAAATGTTGCATG 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 AACAAATGTCATAAATATCTCATAGAGGTACAGTGCCAATAGATATTCAAATGTTGCATG 1560

Qy    1561 TTGACCAGAGGGATTTTATATCTGAAGAACATACACTATTAATAAATACCTTAGAGAAAG 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 TTGACCAGAGGGATTTTATATCTGAAGAACATACACTATTAATAAATACCTTAGAGAAAG 1620

Qy    1621 ATTTTGACCTGGCTTTAGATAAAACTGTGGCAAGAAAAATGTAATGAGCAATATATGGAA 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 ATTTTGACCTGGCTTTAGATAAAACTGTGGCAAGAAAAATGTAATGAGCAATATATGGAA 1680

Qy    1681 ATAAACACACCTTTGTTAAAGATAAAAAAAAA 1712
           ||||||||||||||||||||||||||||||||
Db    1681 ATAAACACACCTTTGTTAAAGATAAAAAAAAA 1712
```

RESULT 2
AAA95787
ID AAA95787 standard; cDNA; 1760 BP.
XX
AC AAA95787;
XX
DT 28-FEB-2001 (first entry)
XX
DE Human immune system molecule cDNA from Incyte clone 1890540.
XX
KW Anti-inflammatory; keratolytic; anti-HIV; anti-allergic; antianaemic;
KW antiarteriosclerotic; antiasthmatic; antidiabetic; nephrotropic; cancer;
KW antigout; dermatological; antithyroid; virucide; hepatotropic; antibody;
KW immunosuppressive; cytostatic; fungicide; protozoacide; antibacterial;
KW gene therapy; diagnostic; immunological disorder; viral infection; ss;
KW bacterial infection; fungal infection; parasitic infection; immunogen.
XX
OS Homo sapiens.
XX
PN WO200060080-A2.
XX
PD 12-OCT-2000.
XX
PF 04-APR-2000; 2000WO-US09072.
XX
PR 05-APR-1999; 99US-0127852.
PR 05-MAY-1999; 99US-0132647.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Yue H, Lal P, Tang YT, Baughn MR, Azimzai Y, Lu DAM;
XX
DR WPI; 2000-665005/64.
DR P-PSDB; AAB15548.
XX
PT New human immune system molecules 1-15 and polynucleotides encoding
PT them useful for diagnosing, treating or preventing e.g. immunological
PT disorders, infections, cell proliferative disorders, microbial
PT infections
XX
PS Claim 4; Page 93; 95pp; English.
XX
CC This sequence represents the cDNA for a human immune system molecule
CC (IMOL) isolated as clone 1890540 from the Incyte BLADTUT07 library.
CC The human IMOLs (AAB15536-B15550) and their encoding polynucleotides
CC (AAA95775-A95789), and compositions comprising them are useful for the
CC diagnosis, treatment or prevention of immunological disorders,
CC infections and cell proliferative disorders, including cancer. The IMOL
CC may be used to treat or prevent disorders associated with decreased
CC expression or activity of IMOL, such as immunological disorders
CC (e.g. inflammation, actinic keratosis, AIDS, Addison's disease),
CC haematopoietic cancer, infections caused by virus (e.g. adenovirus,
CC parvovirus, coronavirus), bacteria (e.g. Staphylococcus, Streptococcus,
CC Shigella), fungi (e.g. Aspergillus, Blastomyces), parasites (e.g.
CC Plasmodium, Trypanosoma, intestinal protozoa), cell proliferative
CC disorders (e.g. actinic keratosis, arteriosclerosis, bursitis), and
CC cancers (e.g. leukemia, melanoma, sarcoma). The peptides are also
CC useful as immunogens for the development of antibodies that
CC specifically recognizes these peptides. The polynucleotides may be used
CC to detect and quantify gene expression in biopsied tissues in which
CC expression of IMOL may be correlated with the disease, as targets in a
CC microarray, to detect differences in gene sequences among normal,
CC carrier and affected individuals, and for screening libraries of
CC compounds in drug screening techniques. Antibodies which specifically
CC bind to IMOL may be used for the diagnosis of disorders characterized
CC by expression of IMOL, or in assays to monitor patients being treated
CC with IMOL or agonists, antagonists, or inhibitors of IMOL.
XX
SQ Sequence 1760 BP; 505 A; 376 C; 395 G; 484 T; 0 other;

Query Match 99.9%; Score 1710.4; DB 21; Length 1760;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1711; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1 GGCATCTGCCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48 GGCATCTGCCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGA 107

Qy      61 GGCTCTGTTGAGAATCATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     108 GGCTCTGTTGAGAATCATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTT 167

Qy     121 TTTCCTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACT 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     168 TTTCCTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACT 227

Qy     181 ACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     228 ACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCC 287

Qy     241 CCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     288 CCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGG 347

Qy     301 AGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     348 AGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCG 407

Qy     361 AGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     408 AGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGA 467

Qy     421 ACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGAT 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     468 ACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGAT 527

Qy     481 TATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     528 TATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATT 587

Qy     541 TGGGGCCCCAGTATCAGGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGT 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     588 TGGGGCCCCAGTATCAGGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGT 647

Qy     601 TGAGGAAGTGTATGTGTACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTA 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     648 TGAGGAAGTGTATGTGTACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTA 707

Qy     661 TGAAATGAAGGGCAAATCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGG 720
```

```
Db     708 TGAAATGAAGGGCAAATCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGG 767

Qy     721 GGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTCCATGGGGACCACCAACGCTTCTC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     768 GGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTCCATGGGGACCACCAACGCTTCTC 827

Qy     781 CACCTTTGCAGGATTCCTGCTCTTTGAAACTAAGTAAATATATGACTAGAATAGCTCCAC 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     828 CACCTTTGCAGGATTCCTGCTCTTTGAAACTAAGTAAATATATGACTAGAATAGCTCCAC 887

Qy     841 TTTGGGGAAGACTTGTAGCTGAGCTGATTTGTTACGATCTGAGGAACATTAAAGTTGAGG 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     888 TTTGGGGAAGACTTGTAGCTGAGCTGATTTGTTACGATCTGAGGAACATTAAAGTTGAGG 947

Qy     901 GTTTTACATTGCTGTATTCAAAAAATTATTGGTTGCAATGTTGTTCACGCTACAGGTACA 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     948 GTTTTACATTGCTGTATTCAAAAAATTATTGGTTGCAATGTTGTTCACGCTACAGGTACA 1007

Qy     961 CCAATAATGTTGGACAATTCAGGGGCTCAGAAGAATCAACCACAAAATAGTCTTCTCAGA 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1008 CCAATAATGTTGGACAATTCAGGGGCTCAGAAGAATCAACCACAAAATAGTCTTCTCAGA 1067

Qy    1021 TGACCTTGACTAATATACTCAGCATCTTTATCACTCTTTCCTTGGCACCTAAAAGATAAT 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1068 TGACCTTGACTAATATACTCAGCATCTTTATCACTCTTTCCTTGGCACCTAAAAGATAAT 1127

Qy    1081 TCTCCTCTGACGCAGGTTGGAAATATTTTTTTCTATCACAGAAGTCATTTGCAAAGAATT 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1128 TCTCCTCTGACGCAGGTTGGAAATATTTTTTTCTATCACAGAAGTCATTTGCAAAGAATT 1187

Qy    1141 TTGACTACTCTGCTTTTAATTTAATACCAGTTTTCAGGAACCCCTGAAGTTTTAAGTTCA 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1188 TTGACTACTCTGCTTTTAATTTAATACCAGTTTTCAGGAACCCCTGAAGTTTTAAGTTCA 1247

Qy    1201 TTATTCTTTATAACATTTGAGAGAATCGGATGTAGTGATATGACAGGGCTGGGGCAAGAA 1260
           |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db    1248 TTATTCTTTATAACATTTGAGAGAATCAGATGTAGTGATATGACAGGGCTGGGGCAAGAA 1307

Qy    1261 CAGGGGCACTAGCTGCCTTATTAGCTAATTTAGTGCCCTCCGTGTTCAGCTTAGCCTTTG 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1308 CAGGGGCACTAGCTGCCTTATTAGCTAATTTAGTGCCCTCCGTGTTCAGCTTAGCCTTTG 1367

Qy    1321 ACCCTTTCCTTTTGATCCACAAAATACATTAAAACTCTGAATTCACATACAATGCTATTT 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1368 ACCCTTTCCTTTTGATCCACAAAATACATTAAAACTCTGAATTCACATACAATGCTATTT 1427

Qy    1381 TAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACCAGTAATGTGGTTGTAATTTTGTGT 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1428 TAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACCAGTAATGTGGTTGTAATTTTGTGT 1487

Qy    1441 ATGTTCCCCCACATCGCCCCCAACTTCGGATGTGGGGTCAGGAGGTTGAGGTTCACTATT 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1488 ATGTTCCCCCACATCGCCCCCAACTTCGGATGTGGGGTCAGGAGGTTGAGGTTCACTATT 1547

Qy    1501 AACAAATGTCATAAATATCTCATAGAGGTACAGTGCCAATAGATATTCAAATGTTGCATG 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1548 AACAAATGTCATAAATATCTCATAGAGGTACAGTGCCAATAGATATTCAAATGTTGCATG 1607

Qy    1561 TTGACCAGAGGGATTTTATATCTGAAGAACATACACTATTAATAAATACCTTAGAGAAAG 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1608 TTGACCAGAGGGATTTTATATCTGAAGAACATACACTATTAATAAATACCTTAGAGAAAG 1667

Qy    1621 ATTTTGACCTGGCTTTAGATAAAACTGTGGCAAGAAAAATGTAATGAGCAATATATGGAA 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1668 ATTTTGACCTGGCTTTAGATAAAACTGTGGCAAGAAAAATGTAATGAGCAATATATGGAA 1727

Qy    1681 ATAAACACACCTTTGTTAAAGATAAAAAAAAA 1712
           ||||||||||||||||||||||||||||||||
Db    1728 ATAAACACACCTTTGTTAAAGATAAAAAAAAA 1759
```

RESULT 3

```
AAC64058
ID   AAC64058 standard; cDNA; 1696 BP.
XX
AC   AAC64058;
XX
DT   19-FEB-2001  (first entry)
XX
DE   Human zacrp3 cDNA, SEQ ID NO:1.
XX
KW   Human zacrp3; adipocyte complement related protein homologue;
KW   ACRP30; C1q domain; collagen-like domain; energy balance modulation;
KW   cellular metabolism; metabolic disorder; obesity; anorexia;
KW   antimicrobial agent; infection; platelet aggregation inhibition;
KW   adhesion; activation; vascular injury; antibacterial; antiviral; ss.
XX
OS   Homo sapiens.
XX
PN   WO200063377-A1.
XX
PD   26-OCT-2000.
XX
PF   19-APR-2000; 2000WO-US10454.
XX
PR   20-APR-1999;   99US-0294943.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Piddington CS,  Bishop PD;
XX
DR   WPI; 2000-665243/64.
DR   P-PSDB; AAB29580.
XX
PT   Novel zacrp3 polypeptides used to treat or prevent bacterial or viral
PT   infections, for wound healing, improving blood flow, and to analyze
PT   energy efficiency in mammals -
XX
PS   Claim 31; Page 107-109; 123pp; English.
XX
CC   The invention relates to the human zacrp3 protein (AAB29580) and to
CC   nucleic acids which encode it (AAC64058, AAC64063). Zacrp3 is a homogue
CC   of adipocyte complement related protein (ACRP30) and contains a
CC   collagen-like domain comprising Gly-Xaa-Xaa or Gly-Xaa-Pro repeats, and a
CC   C-terminal C1q domain comprising 10 beta-strands. The zacrp3 gene is
CC   located on chromosome 5p12. The invention also relates to zacrp3
CC   fragments, fusion proteins containing zacrp3 polypeptides,
CC   zacrp3-specific antibodies, expression constructs and host cells
CC   comprising zacrp3 nucleic acids, and methods of recombinant production of
CC   zacrp3. Human zacrp3, and its agonists and antagonists may be used in the
CC   study and modulation of cellular metabolism and energy balance in
CC   mammals, and may therefore be used to treat disorders such as obesity and
CC   anorexia, and conditions associated with these disorders. Due to its C1q
CC   like domain, zacrp3 and zacrp3-containing fusion proteins may be useful
CC   as antimicrobial agents, promoting lysis or phagocytosis of infectious
CC   organisms such as bacteria or viruses. Zacrp3, its fragments, fusion
CC   proteins, antibodies and activity modulators may also be used to inhibit
CC   collagen-induced platelet aggregation, adhesion, or activation, and may
CC   therefore have potential for promoting blood flow within the vasculature
CC   of a mammal e.g., to treat injury to the vasculature or other collagenous
CC   tissue. Human zacrp3 and its antibodies may additionally be used to study
CC   dimerisation and oligomerisation. The present sequence represents cDNA
CC   encoding human zacrp3.
XX
SQ   Sequence 1696 BP; 482 A; 355 C; 386 G; 473 T; 0 other;

  Query Match           99.1%;  Score 1696;  DB 21;  Length 1696;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1696;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       9 CCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGAGGCTCTGT 68
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGAGGCTCTGT 60

Qy      69 TGAGAATCATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTCCTCC 128
```

```
Db      61 TGAGAATCATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTCCTCC 120

Qy     129 CTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCCAG 188
Db     121 CTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCCAG 180

Qy     189 ACTGCAGTAAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGC 248
Db     181 ACTGCAGTAAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGC 240

Qy     249 CACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTG 308
Db     241 CACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTG 300

Qy     309 GTCATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGC 368
Db     301 GTCATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGC 360

Qy     369 GGGGGCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGA 428
Db     361 GGGGGCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGA 420

Qy     429 TTGCATTCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCA 488
Db     421 TTGCATTCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCA 480

Qy     489 GCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCC 548
Db     481 GCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCC 540

Qy     549 CAGTATCAGGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAG 608
Db     541 CAGTATCAGGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAG 600

Qy     609 TGTATGTGTACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGA 668
Db     601 TGTATGTGTACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGA 660

Qy     669 AGGGCAAATCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGG 728
Db     661 AGGGCAAATCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGG 720

Qy     729 TTTGGCTGCGAATGGGCAATGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTG 788
Db     721 TTTGGCTGCGAATGGGCAATGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTG 780

Qy     789 CAGGATTCCTGCTCTTTGAAACTAAGTAAATATATGACTAGAATAGCTCCACTTTGGGGA 848
Db     781 CAGGATTCCTGCTCTTTGAAACTAAGTAAATATATGACTAGAATAGCTCCACTTTGGGGA 840

Qy     849 AGACTTGTAGCTGAGCTGATTTGTTACGATCTGAGGAACATTAAAGTTGAGGGTTTTACA 908
Db     841 AGACTTGTAGCTGAGCTGATTTGTTACGATCTGAGGAACATTAAAGTTGAGGGTTTTACA 900

Qy     909 TTGCTGTATTCAAAAAATTATTGGTTGCAATGTTGTTCACGCTACAGGTACACCAATAAT 968
Db     901 TTGCTGTATTCAAAAAATTATTGGTTGCAATGTTGTTCACGCTACAGGTACACCAATAAT 960

Qy     969 GTTGGACAATTCAGGGGCTCAGAAGAATCAACCACAAAATAGTCTTCTCAGATGACCTTG 1028
Db     961 GTTGGACAATTCAGGGGCTCAGAAGAATCAACCACAAAATAGTCTTCTCAGATGACCTTG 1020

Qy    1029 ACTAATATACTCAGCATCTTTATCACTCTTTCCTTGGCACCTAAAAGATAATTCTCCTCT 1088
Db    1021 ACTAATATACTCAGCATCTTTATCACTCTTTCCTTGGCACCTAAAAGATAATTCTCCTCT 1080

Qy    1089 GACGCAGGTTGGAAATATTTTTTTCTATCACAGAAGTCATTTGCAAAGAATTTTGACTAC 1148
Db    1081 GACGCAGGTTGGAAATATTTTTTTCTATCACAGAAGTCATTTGCAAAGAATTTTGACTAC 1140

Qy    1149 TCTGCTTTTAATTTAATACCAGTTTTCAGGAACCCCTGAAGTTTTAAGTTCATTATTCTT 1208
Db    1141 TCTGCTTTTAATTTAATACCAGTTTTCAGGAACCCCTGAAGTTTTAAGTTCATTATTCTT 1200

Qy    1209 TATAACATTTGAGAGAATCGGATGTAGTGATATGACAGGGCTGGGGCAAGAACAGGGGCA 1268
Db    1201 TATAACATTTGAGAGAATCGGATGTAGTGATATGACAGGGCTGGGGCAAGAACAGGGGCA 1260

Qy    1269 CTAGCTGCCTTATTAGCTAATTTAGTGCCCTCCGTGTTCAGCTTAGCCTTTGACCCTTTC 1328
Db    1261 CTAGCTGCCTTATTAGCTAATTTAGTGCCCTCCGTGTTCAGCTTAGCCTTTGACCCTTTC 1320

Qy    1329 CTTTTGATCCACAAAATACATTAAAACTCTGAATTCACATACAATGCTATTTTAAAGTCA 1388
Db    1321 CTTTTGATCCACAAAATACATTAAAACTCTGAATTCACATACAATGCTATTTTAAAGTCA 1380

Qy    1389 ATAGATTTTAGCTATAAAGTGCTTGACCAGTAATGTGGTTGTAATTTTGTGTATGTTCCC 1448
Db    1381 ATAGATTTTAGCTATAAAGTGCTTGACCAGTAATGTGGTTGTAATTTTGTGTATGTTCCC 1440

Qy    1449 CCACATCGCCCCCAACTTCGGATGTGGGGTCAGGAGGTTGAGGTTCACTATTAACAAATG 1508
Db    1441 CCACATCGCCCCCAACTTCGGATGTGGGGTCAGGAGGTTGAGGTTCACTATTAACAAATG 1500

Qy    1509 TCATAAATATCTCATAGAGGTACAGTGCCAATAGATATTCAAATGTTGCATGTTGACCAG 1568
Db    1501 TCATAAATATCTCATAGAGGTACAGTGCCAATAGATATTCAAATGTTGCATGTTGACCAG 1560

Qy    1569 AGGGATTTTATATCTGAAGAACATACACTATTAATAAATACCTTAGAGAAAGATTTTGAC 1628
Db    1561 AGGGATTTTATATCTGAAGAACATACACTATTAATAAATACCTTAGAGAAAGATTTTGAC 1620

Qy    1629 CTGGCTTTAGATAAAACTGTGGCAAGAAAAATGTAATGAGCAATATATGGAAATAAACAC 1688
Db    1621 CTGGCTTTAGATAAAACTGTGGCAAGAAAAATGTAATGAGCAATATATGGAAATAAACAC 1680

Qy    1689 ACCTTTGTTAAAGATA 1704
Db    1681 ACCTTTGTTAAAGATA 1696
```

RESULT 4
AAF93874
ID  AAF93874 standard; cDNA; 1709 BP.
XX
AC  AAF93874;
XX
DT  23-MAY-2001 (first entry)
XX
DE  Human cDNA encoding a membrane or secretory protein clone PSEC0232.
XX
KW  Human; secretory protein; membrane protein; vaccine; gene therapy;
KW  rheumatoid arthritis; diabetes; ss.
XX
OS  Homo sapiens.
XX
PN  EP1067182-A2.
XX
PD  10-JAN-2001.
XX
PF  07-JUL-2000; 2000EP-0114090.
XX
PR  08-JUL-1999; 99JP-0194179.
PR  11-JAN-2000; 2000JP-0118775.
PR  02-MAY-2000; 2000JP-0183766.
XX
PA  (HELI-) HELIX RES INST.
XX
PI  Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
XX
DR  WPI; 2001-093989/11.
DR  P-PSDB; AAB88447.
XX
PT  Nucleic acids encoding secretory proteins/membrane proteins, useful in
PT  gene therapy or as candidate target molecules in drug development -

XX
PS Claim 1; SEQ ID 261; 609pp + CD ROM; English.
XX
CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC which encode human secretory or membrane proteins represented by
CC AAB88317 - AAB88419. Included in the invention are primers
CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
CC cDNA sequences of the invention. The invention also includes methods for
CC the production of antibodies directed against the proteins, and cDNA
CC sequences, which can be used in vaccines. The polynucleotide sequences
CC can be used in gene therapy. The polynucleotide sequences and the
CC proteins they encode may be used in the prevention, treatment and
CC diagnosis of diseases associated with inappropriate secretory
CC protein/membrane protein expression. The nucleic acids and complementary
CC sequences may also be used as DNA probes in diagnostic assays
CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
CC presence of similar nucleic acid sequences in samples. They may also be
CC used to study the expression and function of secretory proteins/membrane
CC polypeptides and their role in metabolism. The polypeptides may be used
CC as antigens in the production of antibodies against them and in assays to
CC identify modulators (agonists and antagonists) of expression and
CC activity. The antibodies and antagonists may also be used as therapeutic
CC agents to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of the
CC polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC (ELISA). Examples of diseases which may be treated include rheumatoid
CC arthritis and diabetes.
XX
SQ Sequence 1709 BP; 480 A; 363 C; 390 G; 476 T; 0 other;

Query Match 99.0%; Score 1695.4; DB 22; Length 1709;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1 GGCATCTGCCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGA 60
Db      13 GGCATCTGCCCGAGGAGACCACGCTCCCGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGA 72

Qy      61 GGCTCTGTTGAGAATCATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTT 120
Db      73 GGCTCTGTTGAGAATCATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTT 132

Qy     121 TTTCCTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACT 180
Db     133 TTTCCTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACT 192

Qy     181 ACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCC 240
Db     193 ACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCC 252

Qy     241 CCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGG 300
Db     253 CCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGG 312

Qy     301 AGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCG 360
Db     313 AGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCG 372

Qy     361 AGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGA 420
Db     373 AGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGA 432

Qy     421 ACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGAT 480
Db     433 ACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGAT 492

Qy     481 TATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATT 540
Db     493 TATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATT 552

Qy     541 TGGGGCCCCAGTATCAGGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGT 600
Db     553 TGGGGCCCCAGTATCAGGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGT 612

Qy     601 TGAGGAAGTGTATGTGTACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTA 660
Db     613 TGAGGAAGTGTATGTGTACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTA 672

Qy     661 TGAAATGAAGGGCAAATCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGG 720
Db     673 TGAAATGAAGGGCAAATCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGG 732

Qy     721 GGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTCCATGGGGACCACCAACGCTTCTC 780
Db     733 GGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTCCATGGGGACCACCAACGCTTCTC 792

Qy     781 CACCTTTGCAGGATTCCTGCTCTTTGAAACTAAGTAAATATATGACTAGAATAGCTCCAC 840
Db     793 CACCTTTGCAGGATTCCTGCTCTTTGAAACTAAGTAAATATATGACTAGAATAGCTCCAC 852

Qy     841 TTTGGGGAAGACTTGTAGCTGAGCTGATTTGTTACGATCTGAGGAACATTAAAGTTGAGG 900
Db     853 TTTGGGGAAGACTTGTAGCTGAGCTGATTTGTTACGATCTGAGGAACATTAAAGTTGAGG 912

Qy     901 GTTTTACATTGCTGTATTCAAAAAATTATTGGTTGCAATGTTGTTCACGCTACAGGTACA 960
Db     913 GTTTTACATTGCTGTATTCAAAAAATTATTGGTTGCAATGTTGTTCACGCTACAGGTACA 972

Qy     961 CCAATAATGTTGGACAATTCAGGGGCTCAGAAGAATCAACCACAAAATAGTCTTCTCAGA 1020
Db     973 CCAATAATGTTGGACAATTCAGGGGCTCAGAAGAATCAACCACAAAATAGTCTTCTCAGA 1032

Qy    1021 TGACCTTGACTAATATACTCAGCATCTTTATCACTCTTTCCTTGGCACCTAAAAGATAAT 1080
Db    1033 TGACCTTGACTAATATACTCAGCATCTTTATCACTCTTTCCTTGGCACCTAAAAGATAAT 1092

Qy    1081 TCTCCTCTGACGCAGGTTGGAAATATTTTTTTCTATCACAGAAGTCATTTGCAAAGAATT 1140
Db    1093 TCTCCTCTGACGCAGGTTGGAAATATTTTTTTCTATCACAGAAGTCATTTGCAAAGAATT 1152

Qy    1141 TTGACTACTCTGCTTTTAATTTAATACCAGTTTTCAGGAACCCCTGAAGTTTTAAGTTCA 1200
Db    1153 TTGACTACTCTGCTTTTAATTTAATACCAGTTTTCAGGAACCCCTGAAGTTTTAAGTTCA 1212

Qy    1201 TTATTCTTTATAACATTTGAGAGAATCGGATGTAGTGATATGACAGGGCTGGGGCAAGAA 1260
Db    1213 TTATTCTTTATAACATTTGAGAGAATCGGATGTAGTGATATGACAGGGCTGGGGCAAGAA 1272

Qy    1261 CAGGGGCACTAGCTGCCTTATTAGCTAATTTAGTGCCCTCCGTGTTCAGCTTAGCCTTTG 1320
Db    1273 CAGGGGCACTAGCTGCCTTATTAGCTAATTTAGTGCCCTCCGTGTTCAGCTTAGCCTTTG 1332

Qy    1321 ACCCTTTCCTTTTGATCCACAAAATACATTAAAACTCTGAATTCACATACAATGCTATTT 1380
Db    1333 ACCCTTTCCTTTTGATCCACAAAATACATTAAAACTCTGAATTCACATACAATGCTATTT 1392

Qy    1381 TAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACCAGTAATGTGGTTGTAATTTTGTGT 1440
Db    1393 TAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACCAGTAATGTGGTTGTAATTTTGTGT 1452

Qy    1441 ATGTTCCCCCACATCGCCCCCAACTTCGGATGTGGGGTCAGGAGGTTGAGGTTCACTATT 1500
Db    1453 ATGTTCCCCCACATCGCCCCCAACTTCGGATGTGGGGTCAGGAGGTTGAGGTTCACTATT 1512

Qy    1501 AACAAATGTCATAAATATCTCATAGAGGTACAGTGCCAATAGATATTCAAATGTTGCATG 1560
Db    1513 AACAAATGTCATAAATATCTCATAGAGGTACAGTGCCAATAGATATTCAAATGTTGCATG 1572

Qy    1561 TTGACCAGAGGGATTTTATATCTGAAGAACATACACTATTAATAAATACCTTAGAGAAAG 1620
Db    1573 TTGACCAGAGGGATTTTATATCTGAAGAACATACACTATTAATAAATACCTTAGAGAAAG 1632

Qy    1621 ATTTTGACCTGGCTTTAGATAAAACTGTGGCAAGAAAAATGTAATGAGCAATATATGGAA 1680
Db    1633 ATTTTGACCTGGCTTTAGATAAAACTGTGGCAAGAAAAATGTAATGAGCAATATATGGAA 1692
```

```
Qy   1681 ATAAACACACCTTTGTT 1697
          |||||||||||||||||
Db   1693 ATAAACACACCTTTGTT 1709


RESULT 5
AAI99523
ID   AAI99523 standard; cDNA; 1620 BP.
XX
AC   AAI99523;
XX
DT   07-JAN-2002  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 21.
XX
KW   Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW   antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW   vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW   cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW   neurological disease; infection; human; secreted protein; ss.
XX
OS   Homo sapiens.
XX
PN   WO200155173-A2.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US01356.
XX
PR   31-JAN-2000; 2000US-0179065.
PR   04-FEB-2000; 2000US-0180628.
PR   24-FEB-2000; 2000US-0184664.
PR   02-MAR-2000; 2000US-0186350.
PR   16-MAR-2000; 2000US-0189874.
PR   17-MAR-2000; 2000US-0190076.
PR   18-APR-2000; 2000US-0198123.
PR   19-MAY-2000; 2000US-0205515.
PR   07-JUN-2000; 2000US-0209467.
PR   28-JUN-2000; 2000US-0214886.
PR   30-JUN-2000; 2000US-0215135.
PR   07-JUL-2000; 2000US-0216647.
PR   07-JUL-2000; 2000US-0216880.
PR   11-JUL-2000; 2000US-0217487.
PR   11-JUL-2000; 2000US-0217496.
PR   14-JUL-2000; 2000US-0218290.
PR   26-JUL-2000; 2000US-0220963.
PR   26-JUL-2000; 2000US-0220964.
PR   14-AUG-2000; 2000US-0224518.
PR   14-AUG-2000; 2000US-0224519.
PR   14-AUG-2000; 2000US-0225213.
PR   14-AUG-2000; 2000US-0225214.
PR   14-AUG-2000; 2000US-0225266.
PR   14-AUG-2000; 2000US-0225267.
PR   14-AUG-2000; 2000US-0225268.
PR   14-AUG-2000; 2000US-0225270.
PR   14-AUG-2000; 2000US-0225447.
PR   14-AUG-2000; 2000US-0225757.
PR   14-AUG-2000; 2000US-0225758.
PR   14-AUG-2000; 2000US-0225759.
PR   18-AUG-2000; 2000US-0226279.
PR   22-AUG-2000; 2000US-0226681.
PR   22-AUG-2000; 2000US-0226868.
PR   22-AUG-2000; 2000US-0227182.
PR   23-AUG-2000; 2000US-0227009.
PR   30-AUG-2000; 2000US-0228924.
PR   01-SEP-2000; 2000US-0229287.
PR   01-SEP-2000; 2000US-0229343.
PR   01-SEP-2000; 2000US-0229344.
PR   01-SEP-2000; 2000US-0229345.
PR   05-SEP-2000; 2000US-0229509.
PR   05-SEP-2000; 2000US-0229513.
PR   06-SEP-2000; 2000US-0230437.
PR   06-SEP-2000; 2000US-0230438.
PR   08-SEP-2000; 2000US-0231242.
PR   08-SEP-2000; 2000US-0231243.
PR   08-SEP-2000; 2000US-0231244.
PR   08-SEP-2000; 2000US-0231413.
PR   08-SEP-2000; 2000US-0231414.
PR   08-SEP-2000; 2000US-0232080.
PR   08-SEP-2000; 2000US-0232081.
PR   12-SEP-2000; 2000US-0231968.
PR   14-SEP-2000; 2000US-0232397.
PR   14-SEP-2000; 2000US-0232398.
PR   14-SEP-2000; 2000US-0232399.
PR   14-SEP-2000; 2000US-0232400.
PR   14-SEP-2000; 2000US-0232401.
PR   14-SEP-2000; 2000US-0233063.
PR   14-SEP-2000; 2000US-0233064.
PR   14-SEP-2000; 2000US-0233065.
PR   21-SEP-2000; 2000US-0234223.
PR   21-SEP-2000; 2000US-0234274.
PR   25-SEP-2000; 2000US-0234997.
PR   25-SEP-2000; 2000US-0234998.
PR   26-SEP-2000; 2000US-0235484.
PR   27-SEP-2000; 2000US-0235834.
PR   27-SEP-2000; 2000US-0235836.
PR   29-SEP-2000; 2000US-0236327.
PR   29-SEP-2000; 2000US-0236367.
PR   29-SEP-2000; 2000US-0236368.
PR   29-SEP-2000; 2000US-0236369.
PR   29-SEP-2000; 2000US-0236370.
PR   02-OCT-2000; 2000US-0236802.
PR   02-OCT-2000; 2000US-0237037.
PR   02-OCT-2000; 2000US-0237038.
PR   02-OCT-2000; 2000US-0237039.
PR   02-OCT-2000; 2000US-0237040.
PR   13-OCT-2000; 2000US-0239935.
PR   13-OCT-2000; 2000US-0239937.
PR   20-OCT-2000; 2000US-0240960.
PR   20-OCT-2000; 2000US-0241221.
PR   20-OCT-2000; 2000US-0241785.
PR   20-OCT-2000; 2000US-0241786.
PR   20-OCT-2000; 2000US-0241787.
PR   20-OCT-2000; 2000US-0241808.
PR   20-OCT-2000; 2000US-0241809.
PR   20-OCT-2000; 2000US-0241826.
PR   01-NOV-2000; 2000US-0244617.
PR   08-NOV-2000; 2000US-0246474.
PR   08-NOV-2000; 2000US-0246475.
PR   08-NOV-2000; 2000US-0246476.
PR   08-NOV-2000; 2000US-0246477.
PR   08-NOV-2000; 2000US-0246478.
PR   08-NOV-2000; 2000US-0246523.
PR   08-NOV-2000; 2000US-0246524.
PR   08-NOV-2000; 2000US-0246525.
PR   08-NOV-2000; 2000US-0246526.
PR   08-NOV-2000; 2000US-0246527.
PR   08-NOV-2000; 2000US-0246528.
PR   08-NOV-2000; 2000US-0246532.
PR   08-NOV-2000; 2000US-0246609.
PR   08-NOV-2000; 2000US-0246610.
PR   08-NOV-2000; 2000US-0246611.
PR   08-NOV-2000; 2000US-0246613.
PR   17-NOV-2000; 2000US-0249207.
PR   17-NOV-2000; 2000US-0249208.
PR   17-NOV-2000; 2000US-0249209.
PR   17-NOV-2000; 2000US-0249210.
PR   17-NOV-2000; 2000US-0249211.
PR   17-NOV-2000; 2000US-0249212.
PR   17-NOV-2000; 2000US-0249213.
PR   17-NOV-2000; 2000US-0249214.
PR   17-NOV-2000; 2000US-0249215.
PR   17-NOV-2000; 2000US-0249216.
PR   17-NOV-2000; 2000US-0249217.
PR   17-NOV-2000; 2000US-0249218.
PR   17-NOV-2000; 2000US-0249244.
```

```
PR   17-NOV-2000; 2000US-0249245.
PR   17-NOV-2000; 2000US-0249264.
PR   17-NOV-2000; 2000US-0249265.
PR   17-NOV-2000; 2000US-0249297.
PR   17-NOV-2000; 2000US-0249299.
PR   17-NOV-2000; 2000US-0249300.
PR   01-DEC-2000; 2000US-0250160.
PR   01-DEC-2000; 2000US-0250391.
PR   05-DEC-2000; 2000US-0251030.
PR   05-DEC-2000; 2000US-0251988.
PR   05-DEC-2000; 2000US-0256719.
PR   06-DEC-2000; 2000US-0251479.
PR   08-DEC-2000; 2000US-0251856.
PR   08-DEC-2000; 2000US-0251868.
PR   08-DEC-2000; 2000US-0251869.
PR   08-DEC-2000; 2000US-0251989.
PR   08-DEC-2000; 2000US-0251990.
PR   11-DEC-2000; 2000US-0254097.
PR   05-JAN-2001; 2001US-0259678.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
DR   WPI; 2001-451924/48.
DR   P-PSDB; AAM99925.
XX
PT   New nucleic acids and polypeptides, useful for treating, preventing or
PT   ameliorating human disorders and diseases -
XX
PS   Claim 1; SEQ ID NO 21; 465pp + Sequence Listing; English.
XX
CC   The invention relates to novel human polynucleotides (AAI99513-AAI99538)
CC   and the encoded proteins (AAM99915-AAM99934) which are useful for
CC   preventing, treating or ameliorating medical conditions e.g. by protein
CC   or gene therapy. The genes are isolated from a range of human tissues
CC   disclosed in the specification. The nucleic acids, proteins, antibodies
CC   and (ant)agonists are useful in the diagnosis, treatment and prevention
CC   of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the
CC   adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
CC   lung, or urogenital; (b) immune disorders e.g. Addison's disease,
CC   allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
CC   diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
CC   arthritis and ulcerative colitis; (c) cardiovascular disorders such as
CC   myocardial ischaemias; (d) wound healing; (e) neurological diseases
CC   e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as
CC   viral, bacterial, fungal and parasitic infections.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1620 BP; 485 A; 332 C; 360 G; 440 T; 3 other;

  Query Match             90.5%;  Score 1549.6;  DB 22;  Length 1620;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 1549;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy     159 AGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTACA 218
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      22 AGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTACA 81

Qy     219 GCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACC 278
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      82 GCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACC 141

Qy     279 ATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCG 338
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     142 ATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCG 201

Qy     339 ACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAGG 398
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     202 ACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAGG 261

Qy     399 GCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCACT 458
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     262 GCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCACT 321

Qy     459 TCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTCT 518
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     322 TCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTCT 381

Qy     519 TTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGGTGTGTATTTCTTCACCTTCA 578
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     382 TTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGGTGTGTATTTCTTCACCTTCA 441

Qy     579 GCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATGGCAACA 638
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     442 GCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATGGCAACA 501

Qy     639 CAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCAATCATG 698
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     502 CAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCAATCATG 561

Qy     699 CTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTCC 758
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     562 CTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTCC 621

Qy     759 ATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTAAGTAAA 818
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     622 ATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTAAGTAAA 681

Qy     819 TATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCTGATTTGTTACGAT 878
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     682 TATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCTGATTTGTTACGAT 741

Qy     879 CTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATTATTGGTTGCAA 938
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     742 CTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATTATTGGTTGCAA 801

Qy     939 TGTTGTTCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGAAGAATCA 998
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     802 TGTTGTTCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGAAGAATCA 861

Qy     999 ACCACAAAATAGTCTTCTCAGATGACCTTGACTAATATACTCAGCATCTTTATCACTCTT 1058
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     862 ACCACAAAATAGTCTTCTCAGATGACCTTGACTAATATACTCAGCATCTTTATCACTCTT 921

Qy    1059 TCCTTGGCACCTAAAAGATAATTCTCCTCTGACGCAGGTTGGAAATATTTTTTTCTATCA 1118
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     922 TCCTTGGCACCTAAAAGATAATTCTCCTCTGACGCAGGTTGGAAATATTTTTTTCTATCA 981

Qy    1119 CAGAAGTCATTTGCAAAGAATTTTGACTACTCTGCTTTTAATTTAATACCAGTTTTCAGG 1178
           ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db     982 CAGAAGTCATTTGCAAAGAATTTTGACTRCTCTGCTTTTAATTTAATACCAGTTTTCAGG 1041

Qy    1179 AACCCCTGAAGTTTTAAGTTCATTATTCTTTATAACATTTGAGAGAATCGGATGTAGTGA 1238
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    1042 AACCCCTGAAGTTTTAAGTTCATTATTCTTTATAACATTTGAGAGAATCAGATGTAGTGA 1101

Qy    1239 TATGACAGGGCTGGGGCAAGAACAGGGGCACTAGCTGCCTTATTAGCTAATTTAGTGCCC 1298
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1102 TATGACAGGGCTGGGGCAAGAACAGGGGCACTAGCTGCCTTATTAGCTAATTTAGTGCCC 1161

Qy    1299 TCCGTGTTCAGCTTAGCCTTTGACCCTTTCCTTTTGATCCACAAAATACATTAAAACTCT 1358
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1162 TCCGTGTTCAGCTTAGCCTTTGACCCTTTCCTTTTGATCCACAAAATACATTAAAACTCT 1221

Qy    1359 GAATTCACATACAATGCTATTTTAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACCAG 1418
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1222 GAATTCACATACAATGCTATTTTAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACCAG 1281

Qy    1419 TAATGTGGTTGTAATTTTGTGTATGTTCCCCCACATCGCCCCCAACTTCGGATGTGGGGT 1478
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    1282 TAATGTGGTTGTAATTTTGTGTATGTTCCCCCACATCGCCCCCAACTTCGGATGTGCGGT 1341

Qy    1479 CAGGAGGTTGAGGTTCACTATTAACAAATGTCATAAATATCTCATAGAGGTACAGTGCCA 1538
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1342 CAGGAGGTTGAGGTTCACTATTAACAAATGTCATAAATATCTCATAGAGGTACAGTGCCA 1401

Qy    1539 ATAGATATTCAAATGTTGCATGTTGACCAGAGGGATTTTATATCTGAAGAACATACACTA 1598
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1402 ATAGATATTCAAATGTTGCATGTTGACCAGAGGGATTTTATATCTGAAGAACATACACTA 1461

Qy    1599 TTAATAAATACCTTAGAGAAAGATTTTGACCTGGCTTTAGATAAAACTGTGGCAAGAAAA 1658
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1462 TTAATAAATACCTTAGAGAAAGATTTTGACCTGGCTTTAGATAAAACTGTGGCAAGAAAA 1521

Qy    1659 ATGTAATGAGCAATATATGGAAATAAACACACCTTTGTTAAAGATAAAAAAAAA 1712
          ||||||||||||||||||||||||||||||||||||||||:|:|||||||||
Db    1522 ATGTAATGAGCAATATATGGAAATAAACACACCTTTGTTAAARAWAAAAAAAAA 1575


RESULT 6
AAI59230
ID   AAI59230 standard; cDNA; 1792 BP.
XX
AC   AAI59230;
XX
DT   22-OCT-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 1433.
XX
KW   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia; ss.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US34263.
XX
PR   21-JAN-2000; 2000US-0488725.
PR   25-APR-2000; 2000US-0552317.
PR   09-JUL-2000; 2000US-0598042.
PR   19-JUL-2000; 2000US-0620312.
PR   03-AUG-2000; 2000US-0653450.
PR   14-SEP-2000; 2000US-0662191.
PR   19-OCT-2000; 2000US-0693036.
PR   29-NOV-2000; 2000US-0727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Asundi V,  Chen R,  Ma Y,  Qian XB,  Ren F,  Wang D;
PI   Wang J,  Wang Z,  Wehrman T,  Xu C,  Xue AJ,  Yang Y,  Zhang J;
PI   Zhao QA,  Zhou P,  Goodrich R,  Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   P-PSDB; AAM40074.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders
PT   such as central nervous system injuries -
XX
PS   Claim 1; SEQ ID NO 1433; 10078pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC   the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: Immune system suppression,
CC   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification.
XX
SQ   Sequence 1792 BP; 541 A; 352 C; 393 G; 506 T; 0 other;

  Query Match             90.5%;  Score 1548.6;  DB 22;  Length 1792;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 1551;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy     155 ATGGAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAGAC 214
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     238 AGGGAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAGAC 297

Qy     215 TACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGA 274
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     298 TACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGA 357

Qy     275 AACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAG 334
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     358 AACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAG 417

Qy     335 GGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAG 394
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     418 GGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAG 477

Qy     395 AAGGGCTACCCGGGGGATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAACC 454
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     478 AAGGGCTACCCGGGGGATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAACC 537

Qy     455 CACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAAAC 514
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     538 CACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAAAC 597

Qy     515 TTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGGTGTGTATTTCTTCACC 574
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     598 TTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGGTGTGTATTTCTTCACC 657

Qy     575 TTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATGGC 634
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     658 TTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATGGC 717

Qy     635 AACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCAAT 694
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     718 AACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCAAT 777

Qy     695 CATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCGCT 754
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     778 CATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCGCT 837

Qy     755 CTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTAAG 814
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     838 CTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTAAG 897

Qy     815 TAAATATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCTGATTTGTTA 874
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     898 TAAATATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCTGATTTGTTA 957

Qy     875 CGATCTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATTATTGGTT 934
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     958 CGATCTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATTATTGGTT 1017

Qy     935 GCAATGTTGTTCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGAAGA 994
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1018 GCAATGTTGTTCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGAAGA 1077

Qy     995 ATCAACCACAAAATAGTCTTCTCAGATGACCTTGACTAATATACTCAGCATCTTTATCAC 1054
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1078 ATCAACCACAAAATAGTCTTCTCAGATGACCTTGACTAATATACTCAGCATCTTTATCAC 1137
```

```
Qy    1055 TCTTTCCTTGGCACCTAAAAGATAATTCTCCTCTGACGCAGGTTGGAAATATTTTTTTCT 1114
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1138 TCTTTCCTTGGCACCTAAAAGATAATTCTCCTCTGACGCAGGTTGGAAATATTTTTTTCT 1197

Qy    1115 ATCACAGAAGTCATTTGCAAAGAATTTTGACTACTCTGCTTTTAATTTAATACCAGTTTT 1174
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1198 ATCACAGAAGTCATTTGCAAAGAATTTTGACTACTCTGCTTTTAATTTAATACCAGTTTT 1257

Qy    1175 CAGGAACCCCTGAAGTTTTAAGTTCATTATTCTTTATAACATTTGAGAGAATCGGATGTA 1234
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1258 CAGGAACCCCTGAAGTTTTAAGTTCATTATTCTTTATAACATTTGAGAGAATCGGATGTA 1317

Qy    1235 GTGATATGACAGGGCTGGGGCAAGAACAGGGGCACTAGCTGCCTTATTAGCTAATTTAGT 1294
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1318 GTGATATGACAGGGCTGGGGCAAGAACAGGGGCACTAGCTGCCTTATTAGCTAATTTAGT 1377

Qy    1295 GCCCTCCGTGTTCAGCTTAGCCTTTGACCCTTTCCTTTTGATCCACAAAATACATTAAAA 1354
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1378 GCCCTCCGTGTTCAGCTTAGCCTTTGACCCTTTCCTTTTGATCCACAAAATACATTAAAA 1437

Qy    1355 CTCTGAATTCACATACAATGCTATTTTAAAGTCAATAGATTTTAGCTATAAAGTGCTTGA 1414
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1438 CTCTGAATTCACATACAATGCTATTTTAAAGTCAATAGATTTTAGCTATAAAGTGCTTGA 1497

Qy    1415 CCAGTAATGTGGTTGTAATTTTGTGTATGTTCCCCCACATCGCCCCCAACTTCGGATGTG 1474
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1498 CCAGTAATGTGGTTGTAATTTTGTGTATGTTCCCCCACATCGCCCCCAACTTCGGATGTG 1557

Qy    1475 GGGTCAGGAGGTTGAGGTTCACTATTAACAAATGTCATAAATATCTCATAGAGGTACAGT 1534
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1558 CGGTCAGGAGGTTGAGGTTCACTATTAACAAATGTCATAAATATCTCATAGAGGTACAGT 1617

Qy    1535 GCCAATAGATATTCAAATGTTGCATGTTGACCAGAGGGATTTTATATCTGAAGAACATAC 1594
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1618 GCCAATAGATATTCAAATGTTGCATGTTGACCAGAGGGATTTTATATCTGAAGAACATAC 1677

Qy    1595 ACTATTAATAAATACCTTAGAGAAAGATTTTGACCTGGCTTTAGATAAAACTGTGGCAAG 1654
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1678 ACTATTAATAAATACCTTAGAGAAAGATTTTGACCTGGCTTTAGATAAAACTGTGGCAAG 1737

Qy    1655 AAAAATGTAATGAGCAATATATGGAAATAAACACACCTTTGTTAAAGATAAAAAA 1709
           |||||||||||||||||||||||||||||||||||||||||||||| | ||||||
Db    1738 AAAAATGTAATGAGCAATATATGGAAATAAACACACCTTTGTTAAAAAAAAAAAA 1792
```

RESULT 7
AAD12584
ID AAD12584 standard; cDNA; 1927 BP.
XX
AC AAD12584;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human protein having hydrophobic domain encoding cDNA clone HP10781.
XX
KW Human; hydrophobic domain; gene therapy; nutritional supplement;
KW cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial;
KW multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
KW haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic;
KW Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;
KW haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
KW contraceptive; antiinfertility; antiinflammatory; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 89..760
FT /*tag= a
FT /product= "Human protein having hydrophobic domain"
FT /note= "CDS is specifically is claimed in claim 3"
FT sig_peptide 89..157
FT /*tag= b
FT mat_peptide 158..757
FT /*tag= c
FT /product= "Mature human protein with hydrophobic domain"
XX
PN WO200149728-A2.
XX
PD 12-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-JP09359.
XX
PR 06-JAN-2000; 2000JP-0000585.
PR 06-JAN-2000; 2000JP-0000588.
PR 11-JAN-2000; 2000JP-0002299.
PR 03-FEB-2000; 2000JP-0026862.
PR 03-MAR-2000; 2000JP-0058367.
XX
PA (PROT-) PROTEGENE INC.
PA (SAGA ) SAGAMI CHEM RES CENT.
XX
PI Kato S, Kimura T;
XX
DR WPI; 2001-418355/44.
DR P-PSDB; AAE06589.
XX
PT Human proteins with hydrophobic domains and the nucleic acids encoding
PT them, useful for preventing diagnosing and treating e.g. cancer,
PT Alzheimer's and inflammation -
XX
PS Claim 4; Page 352-354; 563pp; English.
XX
CC The present sequence is human protein with hydrophobic domain encoding
CC cDNA clone HP10781. The polynucleotide and polypeptide of the invention
CC may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate polypeptide expression. The polynucleotides
CC may be used to produce the polypeptide, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the protein. The
CC polynucleotides and its complementary sequences may also be used as DNA
CC probes in diagnostic assays and also used in gene therapy. The
CC polypeptides may also be used as antigens in the production of antibodies
CC and in assays to identify modulators of polypeptide expression and
CC activity. The polypeptides and nucleic acids may be used as nutritional
CC supplements, to modulate cytokine and cell proliferation activity, to
CC modulate immune stimulation or suppression (e.g. for the treatment of
CC microbial infections and autoimmune disorders such as multiple sclerosis,
CC rheumatoid arthritis and insulin-dependent diabetes), to modulate
CC haematopoiesis, to modulate tissue growth activity (e.g. for the
CC treatment of Parkinson's disease, Huntington's disease and Alzheimer's
CC disease), to modulate activin and inhibin activity (e.g. for controlling
CC fertility), to modulate chemotactic and chemokinetic activity, to
CC modulate haemostatic and thrombolytic activity, to modulate receptor
CC ligand activity, to modulate inflammation and to inhibit tumour growth.
XX
SQ Sequence 1927 BP; 550 A; 416 C; 452 G; 509 T; 0 other;

Query Match 89.2%; Score 1527; DB 22; Length 1927;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1538; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
Qy     159 AGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTACA 218
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     390 AGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTACA 449

Qy     219 GCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACC 278
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     450 GCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACC 509

Qy     279 ATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCG 338
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     510 ATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCG 569

Qy     339 ACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAGG 398
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     570 ACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAGG 629
```

```
Qy    399 GCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCACT 458
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    630 GCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCACT 689

Qy    459 TCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTCT 518
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    690 TCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTC- 748

Qy    519 TTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGGTGTGTATTTCTTCACCTTCA 578
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    749 TTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGGTGTGTATTTCTTCACCTTCA 808

Qy    579 GCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATGGCAACA 638
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    809 GCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATGGCAACA 868

Qy    639 CAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCAATCATG 698
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    869 CAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCAATCATG 928

Qy    699 CTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTCC 758
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    929 CTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTCC 988

Qy    759 ATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTAAGTAAA 818
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    989 ATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTAAGTAAA 1048

Qy    819 TATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCTGATTTGTTACGAT 878
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1049 TATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCTGATTTGTTACGAT 1108

Qy    879 CTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATTATTGGTTGCAA 938
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1109 CTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATTATTGGTTGCAA 1168

Qy    939 TGTTGTTCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGAAGAATCA 998
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1169 TGTTGTTCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGAAGAATCA 1228

Qy    999 ACCACAAAATAGTCTTCTCAGATGACCTTGACTAATATACTCAGCATCTTTATCACTCTT 1058
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1229 ACCACAAAATAGTCTTCTCAGATGACCTTGACTAATATACTCAGCATCTTTATCACTCTT 1288

Qy   1059 TCCTTGGCACCTAAAAGATAATTCTCCTCTGACGCAGGTTGGAAATATTTTTTTCTATCA 1118
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1289 TCCTTGGCACCTAAAAGATAATTCTCCTCTGACGCAGGTTGGAAATATTTTTTTCTATCA 1348

Qy   1119 CAGAAGTCATTTGCAAAGAATTTTGACTACTCTGCTTTTAATTTAATACCAGTTTTCAGG 1178
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1349 CAGAAGTCATTTGCAAAGAATTTTGACTACTCTGCTTTTAATTTAATACCAGTTTTCAGG 1408

Qy   1179 AACCCCTGAAGTTTTAAGTTCATTATTCTTTATAACATTTGAGAGAATCGGATGTAGTGA 1238
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1409 AACCCCTGAAGTTTTAAGTTCATTATTCTTTATAACATTTGAGAGAATCGGATGTAGTGA 1468

Qy   1239 TATGACAGGGCTGGGGCAAGAACAGGGGCACTAGCTGCCTTATTAGCTAATTTAGTGCCC 1298
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1469 TATGACAGGGCTGGGGCAAGAACAGGGGCACTAGCTGCCTTATTAGCTAATTTAGTGCCC 1528

Qy   1299 TCCGTGTTCAGCTTAGCCTTTGACCCTTTCCTTTTGATCCACAAAATACATTAAAACTCT 1358
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1529 TCCGTGTTCAGCTTAGCCTTTGACCCTTTCCTTTTGATCCACAAAATACATTAAAACTCT 1588

Qy   1359 GAATTCACATACAATGCTATTTTAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACCAG 1418
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1589 GAATTCACATACAATGCTATTTTAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACCAG 1648

Qy   1419 TAATGTGGTTGTAATTTTGTGTATGTTCCCCCACATCGCCCCCAACTTCGGATGTGGGGT 1478
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1649 TAATGTGGTTGTAATTTTGTGTATGTTCCCCCACATCGCCCCCAACTTCGGATGTGGGGT 1708
```

```
Qy   1479 CAGGAGGTTGAGGTTCACTATTAACAAATGTCATAAATATCTCATAGAGGTACAGTGCCA 1538
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1709 CAGGAGGTTGAGGTTCACTATTAACAAATGTCATAAATATCTCATAGAGGTACAGTGCCA 1768

Qy   1539 ATAGATATTCAAATGTTGCATGTTGACCAGAGGGATTTTATATCTGAAGAACATACACTA 1598
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1769 ATAGATATTCAAATGTTGCATGTTGACCAGAGGGATTTTATATCTGAAGAACATACACTA 1828

Qy   1599 TTAATAAATACCTTAGAGAAAGATTTTGACCTGGCTTTAGATAAAACTGTGGCAAGAAAA 1658
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1829 TTAATAAATACCTTAGAGAAAGATTTTGACCTGGCTTTAGATAAAACTGTGGCAAGAAAA 1888

Qy   1659 ATGTAATGAGCAATATATGGAAATAAACACACCTTTGTT 1697
          |||||||||||||||||||||||||||||||||||||
Db   1889 ATGTAATGAGCAATATATGGAAATAAACACACCTTTGTT 1927
```

RESULT 8
ABK35221
ID  ABK35221 standard; cDNA; 1608 BP.
XX
AC  ABK35221;
XX
DT  08-MAY-2002  (first entry)
XX
DE  Human cDNA encoding secreted protein #359.
XX
KW  Human; secreted protein; gene; ss; nutritional supplement; haemophilia;
KW  viral infection; bacterial infection; fungal infection; diabetes; asthma;
KW  autoimmune disorder; rheumatoid arthritis; multiple sclerosis; tumour;
KW  autoimmune thyroiditis; allergic reaction; neurodegenerative disease;
KW  Alzheimer's disease; Parkinson's disease; liver fibrosis; cancer; ulcer;
KW  coagulation disorder; inflammatory disorder; Crohn's disease; incision;
KW  tissue regeneration; wound healing; burn; haematopoiesis;
KW  myeloid cell deficiency; lymphoid cell deficiency.
XX
OS  Homo sapiens.
XX
PN  WO200177288-A2.
XX
PD  18-OCT-2001.
XX
PF  29-MAR-2001; 2001WO-US10224.
XX
PR  06-APR-2000; 2000US-195582P.
XX
PA  (GEMY ) GENETICS INST INC.
XX
PI  Wong GG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;
PI  Gulukota K, Graham JR;
XX
DR  WPI; 2002-179321/23.
XX
PT  Five hundred and ninety two polynucleotides derived from a variety of
PT  human tissue sources which encode secreted proteins, useful for
PT  treating immune deficiencies and disorders such as autoimmune disorders
PT  -
XX
PS  Claim 1; Page 261-262; 372pp; English.
XX
CC  The invention relates to 592 polynucleotides which have been derived from
CC  a variety of human tissue sources and which encode novel secreted
CC  proteins. The polynucleotides can be used as probes for the
CC  identification and isolation of full length cDNA and genomic DNA. The
CC  polynucleotides and proteins can also be used as nutritional supplements.
CC  The proteins are useful in the treatment of various immune deficiencies
CC  and disorders such as viral infections, bacterial infections, fungal
CC  infections, autoimmune disorders (e.g. rheumatoid arthritis, multiple
CC  sclerosis, autoimmune thyroiditis and diabetes) and allergic reactions
CC  and conditions (e.g. asthma). They are also useful for treating
CC  neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's
CC  disease), liver fibrosis, coagulation disorders (e.g. haemophilia),
CC  inflammatory disorders (e.g. Crohn's disease) and tumours. They are also

```
CC   useful for tissue regeneration, for wound healing and in the treatment of
CC   burns, incisions and ulcers. The proteins are also useful for regulating
CC   haematopoiesis and for treating myeloid or lymphoid cell deficiencies.
CC   Sequences ABK34863-ABK35454 represent polynucleotides of the invention.
XX
SQ   Sequence 1608 BP; 487 A; 305 C; 339 G; 477 T; 0 other;

  Query Match             79.6%;  Score 1363.2;  DB 24;  Length 1608;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1365;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     337 CGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAA 396
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAA 60

Qy     397 GGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCA 456
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCA 120

Qy     457 CTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAAACTT 516
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAAACTT 180

Qy     517 CTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGGTGTGTATTTCTTCACCTT 576
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGGTGTGTATTTCTTCACCTT 240

Qy     577 CAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATGGCAA 636
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATGGCAA 300

Qy     637 CACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCAATCA 696
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCAATCA 360

Qy     697 TGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCT 756
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 TGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCT 420

Qy     757 CCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTAAGTA 816
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTAAGTA 480

Qy     817 AATATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCTGATTTGTTACG 876
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 AATATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCTGATTTGTTACG 540

Qy     877 ATCTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATTATTGGTTGC 936
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 ATCTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATTATTGGTTGC 600

Qy     937 AATGTTGTTCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGAAGAAT 996
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 AATGTTGTTCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGAAGAAT 660

Qy     997 CAACCACAAAATAGTCTTCTCAGATGACCTTGACTAATATACTCAGCATCTTTATCACTC 1056
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CAACCACAAAATAGTCTTCTCAGATGACCTTGACTAATATACTCAGCATCTTTATCACTC 720

Qy    1057 TTTCCTTGGCACCTAAAAGATAATTCTCCTCTGACGCAGGTTGGAAATATTTTTTTCTAT 1116
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 TTTCCTTGGCACCTAAAAGATAATTCTCCTCTGACGCAGGTTGGAAATATTTTTTTCTAT 780

Qy    1117 CACAGAAGTCATTTGCAAAGAATTTTGACTACTCTGCTTTTAATTTAATACCAGTTTTCA 1176
           |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db     781 CACAGAAGTCATTTGCAAAGAATTTTGACTGCTCTGCTTTTAATTTAATACCAGTTTTCA 840

Qy    1177 GGAACCCCTGAAGTTTTAAGTTCATTATTCTTTATAACATTTGAGAGAATCGGATGTAGT 1236
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db     841 GGAACCCCTGAAGTTTTAAGTTCATTATTCTTTATAACATTTGAGAGAATCAGATGTAGT 900

Qy    1237 GATATGACAGGGCTGGGGCAAGAACAGGGGCACTAGCTGCCTTATTAGCTAATTTAGTGC 1296
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GATATGACAGGGCTGGGGCAAGAACAGGGGCACTAGCTGCCTTATTAGCTAATTTAGTGC 960

Qy    1297 CCTCCGTGTTCAGCTTAGCCTTTGACCCTTTCCTTTTGATCCACAAAATACATTAAAACT 1356
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 CCTCCGTGTTCAGCTTAGCCTTTGACCCTTTCCTTTTGATCCACAAAATACATTAAAACT 1020

Qy    1357 CTGAATTCACATACAATGCTATTTTAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACC 1416
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CTGAATTCACATACAATGCTATTTTAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACC 1080

Qy    1417 AGTAATGTGGTTGTAATTTTGTGTATGTTCCCCCACATCGCCCCCAACTTCGGATGTGGG 1476
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    1081 AGTAATGTGGTTGTAATTTTGTGTATGTTCCCCCACATCGCCCCCAACTTCGGATGTGCG 1140

Qy    1477 GTCAGGAGGTTGAGGTTCACTATTAACAAATGTCATAAATATCTCATAGAGGTACAGTGC 1536
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 GTCAGGAGGTTGAGGTTCACTATTAACAAATGTCATAAATATCTCATAGAGGTACAGTGC 1200

Qy    1537 CAATAGATATTCAAATGTTGCATGTTGACCAGAGGGATTTTATATCTGAAGAACATACAC 1596
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 CAATAGATATTCAAATGTTGCATGTTGACCAGAGGGATTTTATATCTGAAGAACATACAC 1260

Qy    1597 TATTAATAAATACCTTAGAGAAAGATTTTGACCTGGCTTTAGATAAAACTGTGGCAAGAA 1656
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TATTAATAAATACCTTAGAGAAAGATTTTGACCTGGCTTTAGATAAAACTGTGGCAAGAA 1320

Qy    1657 AAATGTAATGAGCAATATATGGAAATAAACACACCTTTGTTAAAGATA 1704
           |||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 AAATGTAATGAGCAATATATGGAAATAAACACACCTTTGTTAAAGATA 1368


RESULT 9
AAI61016/c
ID   AAI61016 standard; cDNA; 1799 BP.
XX
AC   AAI61016;
XX
DT   22-OCT-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 5005.
XX
KW   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia; ss.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US34263.
XX
PR   21-JAN-2000; 2000US-0488725.
PR   25-APR-2000; 2000US-0552317.
PR   09-JUL-2000; 2000US-0598042.
PR   19-JUL-2000; 2000US-0620312.
PR   03-AUG-2000; 2000US-0653450.
PR   14-SEP-2000; 2000US-0662191.
PR   19-OCT-2000; 2000US-0693036.
PR   29-NOV-2000; 2000US-0727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Asundi V,  Chen R,  Ma Y,  Qian XB,  Ren F,  Wang D;
PI   Wang J,  Wang Z,  Wehrman T,  Xu C,  Xue AJ,  Yang Y,  Zhang J;
PI   Zhao QA,  Zhou P,  Goodrich R,  Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   P-PSDB; AAM41860.
```

```
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders
PT   such as central nervous system injuries -
XX
PS   Claim 1; SEQ ID NO 5005; 10078pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC   the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: Immune system suppression,
CC   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification.
XX
SQ   Sequence 1799 BP; 531 A; 389 C; 344 G; 535 T; 0 other;

  Query Match             75.7%;  Score 1295.4;  DB 22;  Length 1799;
  Best Local Similarity   93.6%;  Pred. No. 0;
  Matches 1401;  Conservative    0;  Mismatches    1;  Indels   95;  Gaps    1;

Qy     303 CCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAG 362
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1799 CCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAG 1740

Qy     363 GGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAAC 422
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1739 GGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAAC 1680

Qy     423 TT---------------------------------------------------------- 424
           ||
Db    1679 TTCAGGCTGGAGTGCAGTGGTGTGATCTTGGCTCACTGCAGCCTCCACCAAGGTTCAAGC 1620

Qy     425 ------------------------------------CAGATTGCATTCATGGCTTCTCT 447
                                                ||||||||||||||||||||||
Db    1619 GATTCTCTTGCCTCAACCTCTGGAGTAGCTGGGATTACAGATTGCATTCATGGCTTCTCT 1560

Qy     448 GGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACAT 507
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1559 GGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACAT 1500

Qy     508 TGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGGTGTGTATTT 567
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1499 TGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGGTGTGTATTT 1440

Qy     568 CTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCA 627
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1439 CTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCA 1380

Qy     628 CAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATC 687
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1379 CAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATC 1320

Qy     688 CAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAA 747
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1319 CAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAA 1260

Qy     748 TGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGA 807
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1259 TGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGA 1200

Qy     808 AACTAAGTAAATATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCTGA 867
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1199 AACTAAGTAAATATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCTGA 1140

Qy     868 TTTGTTACGATCTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATT 927
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1139 TTTGTTACGATCTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATT 1080

Qy     928 ATTGGTTGCAATGTTGTTCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCT 987
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1079 ATTGGTTGCAATGTTGTTCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCT 1020

Qy     988 CAGAAGAATCAACCACAAAATAGTCTTCTCAGATGACCTTGACTAATATACTCAGCATCT 1047
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1019 CAGAAGAATCAACCACAAAATAGTCTTCTCAGATGACCTTGACTAATATACTCAGCATCT 960

Qy    1048 TTATCACTCTTTCCTTGGCACCTAAAAGATAATTCTCCTCTGACGCAGGTTGGAAATATT 1107
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     959 TTATCACTCTTTCCTTGGCACCTAAAAGATAATTCTCCTCTGACGCAGGTTGGAAATATT 900

Qy    1108 TTTTTCTATCACAGAAGTCATTTGCAAAGAATTTTGACTACTCTGCTTTTAATTTAATAC 1167
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     899 TTTTTCTATCACAGAAGTCATTTGCAAAGAATTTTGACTACTCTGCTTTTAATTTAATAC 840

Qy    1168 CAGTTTTCAGGAACCCCTGAAGTTTTAAGTTCATTATTCTTTATAACATTTGAGAGAATC 1227
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     839 CAGTTTTCAGGAACCCCTGAAGTTTTAAGTTCATTATTCTTTATAACATTTGAGAGAATC 780

Qy    1228 GGATGTAGTGATATGACAGGGCTGGGGCAAGAACAGGGGCACTAGCTGCCTTATTAGCTA 1287
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     779 GGATGTAGTGATATGACAGGGCTGGGGCAAGAACAGGGGCACTAGCTGCCTTATTAGCTA 720

Qy    1288 ATTTAGTGCCCTCCGTGTTCAGCTTAGCCTTTGACCCTTTCCTTTTGATCCACAAAATAC 1347
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     719 ATTTAGTGCCCTCCGTGTTCAGCTTAGCCTTTGACCCTTTCCTTTTGATCCACAAAATAC 660

Qy    1348 ATTAAAACTCTGAATTCACATACAATGCTATTTTAAAGTCAATAGATTTTAGCTATAAAG 1407
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     659 ATTAAAACTCTGAATTCACATACAATGCTATTTTAAAGTCAATAGATTTTAGCTATAAAG 600

Qy    1408 TGCTTGACCAGTAATGTGGTTGTAATTTTGTGTATGTTCCCCCACATCGCCCCCAACTTC 1467
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     599 TGCTTGACCAGTAATGTGGTTGTAATTTTGTGTATGTTCCCCCACATCGCCCCCAACTTC 540

Qy    1468 GGATGTGGGGTCAGGAGGTTGAGGTTCACTATTAACAAATGTCATAAATATCTCATAGAG 1527
           |||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     539 GGATGTGCGGTCAGGAGGTTGAGGTTCACTATTAACAAATGTCATAAATATCTCATAGAG 480

Qy    1528 GTACAGTGCCAATAGATATTCAAATGTTGCATGTTGACCAGAGGGATTTTATATCTGAAG 1587
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     479 GTACAGTGCCAATAGATATTCAAATGTTGCATGTTGACCAGAGGGATTTTATATCTGAAG 420

Qy    1588 AACATACACTATTAATAAATACCTTAGAGAAAGATTTTGACCTGGCTTTAGATAAAACTG 1647
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     419 AACATACACTATTAATAAATACCTTAGAGAAAGATTTTGACCTGGCTTTAGATAAAACTG 360

Qy    1648 TGGCAAGAAAAATGTAATGAGCAATATATGGAAATAAACACACCTTTGTTAAAGATA 1704
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     359 TGGCAAGAAAAATGTAATGAGCAATATATGGAAATAAACACACCTTTGTTAAAGATA 303


RESULT 10
AAF94076
ID   AAF94076 standard; DNA; 810 BP.
XX
AC   AAF94076;
XX
DT   23-MAY-2001  (first entry)
XX
DE   Primer specific for DNA encoding secretory/membrane protein SEQ ID 510.
XX
KW   Human; secretory protein; membrane protein; vaccine; gene therapy;
KW   rheumatoid arthritis; diabetes; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   EP1067182-A2.
```

```
XX
PD   10-JAN-2001.
XX
PF   07-JUL-2000; 2000EP-0114090.
XX
PR   08-JUL-1999;   99JP-0194179.
PR   11-JAN-2000; 2000JP-0118775.
PR   02-MAY-2000; 2000JP-0183766.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Kawai Y,  Sugiyama T,  Hayashi K;
XX
DR   WPI; 2001-093989/11.
XX
PT   Nucleic acids encoding secretory proteins/membrane proteins, useful in
PT   gene therapy or as candidate target molecules in drug development -
XX
PS   Claim 4; SEQ ID 510; 609pp + CD ROM; English.
XX
CC   This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC   which encode human secretory or membrane proteins represented by
CC   AAB88317 - AAB88419. Included in the invention are primers
CC   AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
CC   cDNA sequences of the invention. The invention also includes methods for
CC   the production of antibodies directed against the proteins, and cDNA
CC   sequences, which can be used in vaccines. The polynucleotide sequences
CC   can be used in gene therapy. The polynucleotide sequences and the
CC   proteins they encode may be used in the prevention, treatment and
CC   diagnosis of diseases associated with inappropriate secretory
CC   protein/membrane protein expression. The nucleic acids and complementary
CC   sequences may also be used as DNA probes in diagnostic assays
CC   (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
CC   presence of similar nucleic acid sequences in samples. They may also be
CC   used to study the expression and function of secretory proteins/membrane
CC   polypeptides and their role in metabolism. The polypeptides may be used
CC   as antigens in the production of antibodies against them and in assays to
CC   identify modulators (agonists and antagonists) of expression and
CC   activity. The antibodies and antagonists may also be used as therapeutic
CC   agents to down regulate expression and activity. The antibodies may also
CC   be used as diagnostic agents for detecting the presence of the
CC   polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC   (ELISA). Examples of diseases which may be treated include rheumatoid
CC   arthritis and diabetes.
XX
SQ   Sequence 810 BP; 200 A; 201 C; 218 G; 188 T; 3 other;

  Query Match           44.8%;  Score 766.6;  DB 22;  Length 810;
  Best Local Similarity  98.9%;  Pred. No. 1.3e-212;
  Matches  791;  Conservative    0;  Mismatches    7;  Indels    2;  Gaps    2;

Qy      1 GGCATCTGCCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGA 60
          ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db     13 GGCATCTGCCCGAGGAGACCACGCTCCCGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGA 72

Qy     61 GGCTCTGTTGAGAATCATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     73 GGCTCTGTTGAGAATCATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTT 132

Qy    121 TTTCCTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    133 TTTCCTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACT 192

Qy    181 ACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    193 ACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCC 252

Qy    241 CCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    253 CCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGG 312

Qy    301 AGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    313 AGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCG 372

Qy    361 AGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGA 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    373 AGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGA 432

Qy    421 ACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGAT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    433 ACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGAT 492

Qy    481 TATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    493 TATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATT 552

Qy    541 TGGGGCCCCAGTATCAGGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    553 TGGGGCCCCAGTATCAGGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGT 612

Qy    601 TGAGGAAGTGTATGTGTACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTA 660
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    613 TGAGGAAGTGTATGTGTACCTTATGCACAATGGCAACACAGTCTTCAACATGTACAGCTA 672

Qy    661 TGAAATGAAGGGCAAATCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGG 720
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||| |
Db    673 TGAAATGAAGGGCAAATCAGATACATCCAGCAATCATGCTGTGCTGAA-CTAGCCAAANG 731

Qy    721 GGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTCCATGGGGACCACCAACGCTTCTC 780
          |||||||||||||||| ||| |||||||||||| | ||||||||||||||||||||||||
Db    732 GGATGAGGTTTGGCTGCNAAT-GGCAATGGCGCTNTTCATGGGGACCACCAACGCTTCTT 790

Qy    781 CACCTTTGCAGGATTCCTGC 800
          ||||||||||||||||||||
Db    791 CACCTTTGCAGGATTCCTGC 810


RESULT 11
ABK35591
ID   ABK35591 standard; DNA; 741 BP.
XX
AC   ABK35591;
XX
DT   08-MAY-2002  (first entry)
XX
DE   Gene encoding novel human secreted or membrane-associated protein #10.
XX
KW   Human; secreted protein; membrane-associated protein; hypertension;
KW   inflammatory disorder; neurological disorder; haematopoietic disorder;
KW   skeletal developmental disorder; growth abnormality; autoimmune disorder;
KW   neurodegenerative disorder; nervous system disorder; bacterial infection;
KW   peripheral myelinopathy; viral infection; cancer; obesity; diabetes;
KW   hypotension; sexual development disorder; blood disorder; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200204600-A2.
XX
PD   17-JAN-2002.
XX
PF   12-JUL-2001; 2001WO-US21985.
XX
PR   12-JUL-2000; 2000US-218033P.
PR   21-AUG-2000; 2000US-226517P.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
PA   (GLAX ) GLAXO GROUP LTD.
XX
PI   Agarwal P,  Cogswell JP,  Lai Y,  Martensen SA,  Rizvi SK,  Strum JC;
PI   Smith RF,  Xiang Z,  Xie Q;
XX
DR   WPI; 2002-188468/24.
DR   P-PSDB; AAU84371.
XX
```

```
PT   Novel secreted and membrane-associated polypeptides and polynucleotides
PT   encoding the polypeptides, for preventing, treating and ameliorating
PT   cancers, mental or sexual developmental disorders, and malignant tumours
PT   -
XX
PS   Claim 2; Page 106; 151pp; English.
XX
CC   The present invention relates to the isolation of novel human secreted
CC   or membrane-associated proteins and the genes encoding them. The
CC   sequences of the invention are useful for treating, preventing and
CC   ameliorating various diseases such as inflammatory disorders (e.g.
CC   asthma), neurological disorders (e.g. dementia), haematopoietic
CC   disorders, skeletal developmental disorders, growth abnormalities,
CC   neurodegenerative disorders (e.g. Huntington's disease), nervous system
CC   disorders, autoimmune disorders (e.g. rheumatoid arthritis),
CC   peripheral myelinopathies, viral and bacterial infections,
CC   alpha-mannosidosis, diabetes, cancers, malignant tumours, hyper- and
CC   hypotension, obesity, bulimia, anorexia, manic depression, delirium,
CC   mental retardation, Tourette's syndrome, schizophrenia, growth, mental
CC   or sexual development disorders, and dysfunctions of the blood cascade
CC   system including those leading to stroke. ABK35582-ABK35609 represent
CC   the genes encoding the novel human secreted or membrane-associated
CC   proteins of the invention.
XX
SQ   Sequence 741 BP; 191 A; 178 C; 200 G; 172 T; 0 other;

  Query Match             43.3%;  Score 741;  DB 24;  Length 741;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-205;
  Matches  741;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      77 ATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTCCTCCCTTTTTGC 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTCCTCCCTTTTTGC 60

Qy     137 CTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGT 196
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGT 120

Qy     197 AAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGC 256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGC 180

Qy     257 CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAA 316
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAA 240

Qy     317 GGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAG 376
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAG 300

Qy     377 CATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTC 436
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTC 360

Qy     437 ATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTT 496
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 ATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTT 420

Qy     497 GAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCA 556
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCA 480

Qy     557 GGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTG 616
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTG 540

Qy     617 TACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAA 676
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 TACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAA 600

Qy     677 TCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTG 736
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTG 660

Qy     737 CGAATGGGCAATGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTC 796
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CGAATGGGCAATGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTC 720

Qy     797 CTGCTCTTTGAAACTAAGTAA 817
           |||||||||||||||||||||
Db     721 CTGCTCTTTGAAACTAAGTAA 741


RESULT 12
AAC99776
ID   AAC99776 standard; cDNA; 1035 BP.
XX
AC   AAC99776;
XX
DT   08-MAR-2001  (first entry)
XX
DE   Skin cell cDNA, SEQ ID NO: 424.
XX
KW   Rat; skin cell; cytostatic; antiinflammatory; anti-HIV;
KW   nootropic; neuroprotective; vulnerary; immunomodulatory; vaccine;
KW   keratinocyte growth stimulation; cancer; angiogenesis inhibition;
KW   inflammation; neurological disease; ss.
XX
OS   Rattus sp.
XX
PN   WO200069884-A2.
XX
PD   23-NOV-2000.
XX
PF   15-MAY-2000; 2000WO-NZ00075.
XX
PR   14-MAY-1999;   99US-0312283.
XX
PA   (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI   Watson JD,  Strachan L,  Onrust R,  Sleeman M,  Kumble KD,  Murison JG;
XX
DR   WPI; 2001-007495/01.
DR   P-PSDB; AAB55908.
XX
PT   New isolated polynucleotide used in the identification of genetic
PT   disorders and encoding polypeptides used for treating inflammatory
PT   disease, cancer and neurological diseases -
XX
PS   Claim 1; Page 317-318; 352pp; English.
XX
CC   The present polynucleotide encodes a polypeptide which is expressed in
CC   mammalian skin cells. The polypeptide is useful for stimulating
CC   keratinocyte growth and motility, inhibiting the growth of cancer cells,
CC   modulating angiogenesis, inhibiting angiogenesis and vascularisation of
CC   tumours, modulating skin inflammation, stimulating the growth of
CC   epithelial cells, inhibiting the binding of human immunodeficiency virus
CC   (HIV)-1 to leukocytes, and treating inflammmatory disease, cancer and
CC   neurological diseases. The polynucleotide can be used as a marker, in
CC   the identification of genetic disorders, and for the design of
CC   oligonucleotides for examining expression patterns.
XX
SQ   Sequence 1035 BP; 255 A; 242 C; 298 G; 240 T; 0 other;

  Query Match             40.7%;  Score 696.2;  DB 22;  Length 1035;
  Best Local Similarity   82.8%;  Pred. No. 5.1e-192;
  Matches  819;  Conservative    0;  Mismatches  168;  Indels    2;  Gaps    2;

Qy      33 CTCTGCTGTCTTCTCAGGGAGACTCTGAGGCTCTGTTGAGAATCATGCTTTGGAGGCAGC 92
           | |  | |  | | | |||||| ||||  | | |||   ||  ||||||  |||||||||
Db      48 CCCATCAGCTTCCCCGGGGAGATTCTGCCGATTTGTCACGAGCCATGCTCAGGAGGCAGC 107

Qy      93 TCATCTATTGGCAACTGCTGGCTTTGTTTTTCCTCCCTTTTTGCCTGTGTCAAGATGAAT 152
           || |||  ||||| ||||||||||| |||||||||| ||||||||||||||||||||||||
Db     108 TCGTCTGGTGGCACCTGCTGGCTTTGCTTTTCCTCCCATTTTGCCTGTGTCAAGATGAAT 167
```

```
Qy     153 ACATGGAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAG 212
           |||||||||||||||| | |||||||| |||||||||||||| |||||||| |||||||
Db     168 ACATGGAGTCTCCACAAGCTGGAGGACTGCCCCCAGACTGCAGCAAGTGTTGCCATGGAG 227

Qy     213 ACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAG 272
           | ||  | || || || |||||||| |||||||| || || || ||||||||||||||||
Db     228 ATTATGGATTCCGTGGTTACCAAGGGCCCCCTGGACCCCCAGGTCCTCCTGGCATTCCAG 287

Qy     273 GAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGA 332
           |||||||||||||||||| || || |||||||||||| || ||||| ||||| |||||||
Db     288 GAAACCATGGAAACAATGGAAATAACGGAGCCACTGGCCACGAAGGGGCCAAGGGTGAGA 347

Qy     333 AGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAGCATGGCCCCAAAGGAG 392
           | || |||||||| |||||||||||||||||||| ||||||||||||||||||||||||
Db     348 AAGGAGACAAAGGCGACCTGGGGCCTCGAGGGGAACGGGGGCAGCATGGCCCCAAAGGAT 407

Qy     393 AGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAA 452
           ||||||| ||||| ||| | |||||||| || |||||||| |||||||||||||| || |
Db     408 AGAAGGGATACCCAGGGGTGCCACCAGAGCTGCAGATTGCGTTCATGGCTTCTCTAGCGA 467

Qy     453 CCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAA 512
           | ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db     468 CTCACTTCAGCAATCAGAACAGTGGCATTATCTTCAGCAGTGTTGAGACCAACATTGGAA 527

Qy     513 ACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGGTGTGTATTTCTTCA 572
           ||||||| |||||||||||||||||||||||||||| |||||||| ||||||||||||||
Db     528 ACTTCTTCGATGTCATGACTGGTAGATTTGGGGCCCCCGTATCAGGCGTGTATTTCTTCA 587

Qy     573 CCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATG 632
           |||||||||||||||||||||||| || ||||||||||||||||||||||||||||||||
Db     588 CCTTCAGCATGATGAAGCATGAGGACGTGGAGGAAGTGTATGTGTACCTTATGCACAATG 647

Qy     633 GCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCA 692
           | ||||| || |||||||||||||||||||||||  ||||| ||||||||||||||||||
Db     648 GTAACACGGTGTTCAGCATGTACAGCTATGAAACAAAGGGAAAATCAGATACATCCAGCA 707

Qy     693 ATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCG 752
           | ||||| |||||||||  | |||||||| ||||| || |||||  |||||||||| || |
Db     708 ACCATGCAGTGCTGAAGTTGGCCAAAGGAGATGAAGTCTGGCTAAGAATGGGCAACGGTG 767

Qy     753 CTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTA 812
           | |||||||||||||||| |||||||| ||||| ||||| || ||||| ||||||||||
Db     768 CCCTCCATGGGGACCACCAGCGCTTCTCTACCTTCGCAGGCTTTCTGCTTTTTGAAACTA 827

Qy     813 AGTAAATATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCT-GATTTG 871
           ||| | |       || |||||||||   |  ||  || |||||| |||||| |  |||
Db     828 AGTGATGAGGAAGTCAGGATAGCTCCATGCTAAGGGCGATTTGTAGGTGAGCTAGGGTTG 887

Qy     872 TTACGATCTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATTATTG 931
           ||| |||||||||    ||  ||||| || || |  || |     || |       ||||
Db     888 TTAGGATCTGAGGGGTGTTGGAGTTG-GGCTTCTCTATGGAGTATTTAACTGTTACATTG 946

Qy     932 GTTGCAATGTTGTTCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGA 991
           ||  || || |  |||  |||  || | |||||| |||||||| | || |||||||  ||
Db     947 GTCACACTGCTACTCATTCTAATGGCATACCAATTATGTTGGATACTTTAGGGGCTAGGA 1006

Qy     992 AGAATCAACCACAAAATAGTCTTCTCAGA 1020
           |||||  |||||||  || | ||| ||||
Db    1007 AGAATAGACCACAAGGTAATATTCCCAGA 1035
```

RESULT 13
ABL34928
ID  ABL34928 standard; cDNA; 1035 BP.
XX
AC  ABL34928;
XX
DT  04-APR-2002  (first entry)
XX
DE  Rat cDNA isolated from skin cells SEQ ID NO: 424.
XX
KW  Human; rat; mouse; skin cell; skin wound; cancer; growth defect;
KW  developmental defect; inflammatory disease; dermatological; vulnerary;
KW  immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene;
KW  ss.
XX
OS  Rattus sp.
XX
PN  WO200190357-A1.
XX
PD  29-NOV-2001.
XX
PF  24-MAY-2001; 2001WO-NZ00099.
XX
PR  24-MAY-2000; 2000US-206650P.
PR  25-JUL-2000; 2000US-221232P.
XX
PA  (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI  Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG, Kumble KD;
XX
DR  WPI; 2002-122020/16.
XX
PT  New polynucleotides and polypeptides encoded by the polynucleotides
PT  isolated from skin cells, useful for treating skin wounds, cancers,
PT  growth and developmental defects, inflammatory diseases, or for
PT  modulating immune responses
XX
PS  Claim 1; Page 262; 466pp; English.
XX
CC  The present invention provides the protein and coding sequences of cDNAs
CC  isolated from human, murine and rat skin cell libraries. The sequences
CC  can be used in the development of therapeutic agents useful in the
CC  treatment of skin diseases, including skin wounds, cancer, growth
CC  defects, developmental defects and inflammatory diseases. The proteins
CC  have important roles in the induction of hair growth, cell proliferation
CC  and cell-cell interaction, in maintaining tissue integrity, in wound
CC  healing and in modulating immune responses. The present sequence is a
CC  cDNA of the invention.
XX
SQ  Sequence 1035 BP; 255 A; 242 C; 298 G; 240 T; 0 other;

Query Match  40.7%; Score 696.2; DB 24; Length 1035;
Best Local Similarity  82.8%; Pred. No. 5.1e-192;
Matches  819; Conservative  0; Mismatches  168; Indels  2; Gaps  2;

```
Qy      33 CTCTGCTGTCTTCTCAGGGAGACTCTGAGGCTCTGTTGAGAATCATGCTTTGGAGGCAGC 92
           | |  | |  | | | |||||| ||||  | | |||   ||  ||||||  |||||||||
Db      48 CCCATCAGCTTCCCCGGGGAGATTCTGCCGATTTGTCACGAGCCATGCTCAGGAGGCAGC 107

Qy      93 TCATCTATTGGCAACTGCTGGCTTTGTTTTTCCTCCCTTTTTGCCTGTGTCAAGATGAAT 152
           || |||  ||||| |||||||||||| |||||||||| |||||||||||||||||||||||
Db     108 TCGTCTGGTGGCACCTGCTGGCTTTGCTTTTCCTCCCATTTTGCCTGTGTCAAGATGAAT 167

Qy     153 ACATGGAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAG 212
           |||||||||||||||| | |||||||| |||||||||||||| |||||||| |||||||
Db     168 ACATGGAGTCTCCACAAGCTGGAGGACTGCCCCCAGACTGCAGCAAGTGTTGCCATGGAG 227

Qy     213 ACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAG 272
           | ||  | || || || |||||||| |||||||| || || || ||||||||||||||||
Db     228 ATTATGGATTCCGTGGTTACCAAGGGCCCCCTGGACCCCCAGGTCCTCCTGGCATTCCAG 287

Qy     273 GAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGA 332
           |||||||||||||||||| || || |||||||||||| || ||||| ||||| |||||||
Db     288 GAAACCATGGAAACAATGGAAATAACGGAGCCACTGGCCACGAAGGGGCCAAGGGTGAGA 347

Qy     333 AGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAGCATGGCCCCAAAGGAG 392
           | || |||||||| |||||||||||||||||||| ||||||||||||||||||||||||
Db     348 AAGGAGACAAAGGCGACCTGGGGCCTCGAGGGGAACGGGGGCAGCATGGCCCCAAAGGAT 407

Qy     393 AGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAA 452
           ||||||| ||||| ||| | |||||||| || |||||||| |||||||||||||| || |
Db     408 AGAAGGGATACCCAGGGGTGCCACCAGAGCTGCAGATTGCGTTCATGGCTTCTCTAGCGA 467

Qy     453 CCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAA 512
           | ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
```

```
Db     468 CTCACTTCAGCAATCAGAACAGTGGCATTATCTTCAGCAGTGTTGAGACCAACATTGGAA 527

Qy     513 ACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGGTGTGTATTTCTTCA 572
           ||||||| ||||||||||||||||||||||||||||||| |||||||| ||||||||||||
Db     528 ACTTCTTCGATGTCATGACTGGTAGATTTGGGGCCCCCGTATCAGGCGTGTATTTCTTCA 587

Qy     573 CCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATG 632
           |||||||||||||||||||||||| || ||||||||||||||||||||||||||||||||
Db     588 CCTTCAGCATGATGAAGCATGAGGACGTGGAGGAAGTGTATGTGTACCTTATGCACAATG 647

Qy     633 GCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCA 692
           | ||||| || ||||||||||||||||||||||  ||||| ||||||||||||||||||||
Db     648 GTAACACGGTGTTCAGCATGTACAGCTATGAAACAAAGGGAAAATCAGATACATCCAGCA 707

Qy     693 ATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCG 752
           | ||||| |||||||||| | |||||||| ||||| || |||||  |||||||||| || |
Db     708 ACCATGCAGTGCTGAAGTTGGCCAAAGGAGATGAAGTCTGGCTAAGAATGGGCAACGGTG 767

Qy     753 CTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTA 812
           | |||||||||||||||||| |||||||| ||||| ||||| || |||||  ||||||||||
Db     768 CCCTCCATGGGGACCACCAGCGCTTCTCTACCTTCGCAGGCTTTCTGCTTTTTGAAACTA 827

Qy     813 AGTAAATATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCT-GATTTG 871
           ||| |  |       || |||||||||   |  ||  || ||||||  |||||| |  |||
Db     828 AGTGATGAGGAAGTCAGGATAGCTCCATGCTAAGGGCGATTTGTAGGTGAGCTAGGGTTG 887

Qy     872 TTACGATCTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATTATTG 931
           ||| |||||||||    ||  ||||| || || |  || |     || |       ||||
Db     888 TTAGGATCTGAGGGGTGTTGGAGTTG-GGCTTCTCTATGGAGTATTTAACTGTTACATTG 946

Qy     932 GTTGCAATGTTGTTCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGA 991
           ||  || || |  |||  |||  || | |||||| |||||||| | || |||||||  ||
Db     947 GTCACACTGCTACTCATTCTAATGGCATACCAATTATGTTGGATACTTTAGGGGCTAGGA 1006

Qy     992 AGAATCAACCACAAAATAGTCTTCTCAGA 1020
           |||||  |||||||  || | ||| ||||
Db    1007 AGAATAGACCACAAGGTAATATTCCCAGA 1035
```

RESULT 14
AAZ61633
ID AAZ61633 standard; cDNA; 1123 BP.
XX
AC AAZ61633;
XX
DT 27-MAR-2000 (first entry)
XX
DE cDNA encoding rat skin cell secreted protein, SEQ ID NO:28.
XX
KW Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast;
KW embryonic skin cell; keratinocyte stem cell; transit amplifying cell;
KW secreted; transmembrane; inflammation; cancer; neurological disease;
KW angiogenesis; tumour vascularisation; growth disorder;
KW developmental disorder; skin wound; hair follicle disorder;
KW anti-inflammatory; cytostatic; neuroprotective; vulnery; ss.
XX
OS Rattus sp.
XX
PN WO9955865-A1.
XX
PD 04-NOV-1999.
XX
PF 29-APR-1999; 99WO-NZ00051.
XX
PR 29-APR-1998; 98US-0069726.
PR 09-NOV-1998; 98US-0188930.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Strachan L, Sleeman M, Watson JD, Onrust R, Kumble A, Murison JG;
XX
DR WPI; 2000-072177/06.
XX
PT Novel polynucleotides useful for the treatment of various conditions
PT including wounds and cancer -
XX
PS Claim 1; Page 73; 235pp; English.
XX
CC The invention relates to novel nucleic acid sequences derived from rat
CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,
CC and mouse embryonic skin, keratinocyte stem cells and transit amplifying
CC cells. Polypeptides of the invention may be used to treat inflammation,
CC cancer and neurological diseases. The proteins may be used to stimulate
CC the growth and motility of keratinocytes, to inhibit the growth of
CC cancer cells, to modulate angiogenesis and tumour vascularisation, to
CC modulate skin inflammation, to modulate epithelial cell growth and to
CC inhibit binding of HIV-1 to leukocytes. The invention may also be used
CC to treat growth and developmental defects, skin wounds and hair follicle
CC disorders. Sequences AAZ61606-Z61832 represent cDNA sequences derived
CC from several mouse, rat or human skin cell types. Sequences
CC AAZ61606-Z61649, AAZ61725-Z61765, AAZ61802-Z61811 and AAZ61826 encode
CC proteins with an N-terminal signal sequence, indicating that the proteins
CC are secreted. Sequences AAZ61650-Z61668, AAZ61766-Z61780, AAZ61812-Z61817
CC and AAZ61827-Z61829 encode proteins with one or more putative
CC transmembrane domains.
XX
SQ Sequence 1123 BP; 277 A; 266 C; 321 G; 258 T; 1 other;

Query Match 40.7%; Score 696.2; DB 21; Length 1123;
Best Local Similarity 82.8%; Pred. No. 5.3e-192;
Matches 819; Conservative 0; Mismatches 168; Indels 2; Gaps 2;

```
Qy      33 CTCTGCTGTCTTCTCAGGGAGACTCTGAGGCTCTGTTGAGAATCATGCTTTGGAGGCAGC 92
           | |  | |  | | | | |||||| ||||  | | |||   ||  ||||||  |||||||||
Db     136 CCCATCAGCTTCCCCGGGGAGATTCTGCCGATTTGTCACGAGCCATGCTCAGGAGGCAGC 195

Qy      93 TCATCTATTGGCAACTGCTGGCTTTGTTTTTCCTCCCTTTTTGCCTGTGTCAAGATGAAT 152
           || |||  ||||| |||||||||||| |||||||||| ||||||||||||||||||||||
Db     196 TCGTCTGGTGGCACCTGCTGGCTTTGCTTTTCCTCCCATTTTGCCTGTGTCAAGATGAAT 255

Qy     153 ACATGGAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAG 212
           |||||||||||||||| | |||||||| |||||||||||||| |||||||| |||||||
Db     256 ACATGGAGTCTCCACAAGCTGGAGGACTGCCCCCAGACTGCAGCAAGTGTTGCCATGGAG 315

Qy     213 ACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAG 272
           | ||  | || || || |||||||| |||||||| || || || ||||||||||||||||
Db     316 ATTATGGATTCCGTGGTTACCAAGGGCCCCCTGGACCCCCAGGTCCTCCTGGCATTCCAG 375

Qy     273 GAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGA 332
           |||||||||||||||||| || || |||||||||| || ||||| ||||| |||||||
Db     376 GAAACCATGGAAACAATGGAAATAACGGAGCCACTGGCCACGAAGGGGCCAAGGGTGAGA 435

Qy     333 AGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAGCATGGCCCCAAAGGAG 392
           | || |||||||| |||||||||||||||||||| ||||||||||||||||||||||||
Db     436 AAGGAGACAAAGGCGACCTGGGGCCTCGAGGGGAACGGGGGCAGCATGGCCCCAAAGGAT 495

Qy     393 AGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAA 452
           ||||||| ||||| ||| | |||||||| || |||||||| ||||||||||||||| || |
Db     496 AGAAGGGATACCCAGGGGTGCCACCAGAGCTGCAGATTGCGTTCATGGCTTCTCTAGCGA 555

Qy     453 CCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAA 512
           | |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db     556 CTCACTTCAGCAATCAGAACAGTGGCATTATCTTCAGCAGTGTTGAGACCAACATTGGAA 615

Qy     513 ACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGGTGTGTATTTCTTCA 572
           ||||||| |||||||||||||||||||||||||| |||||||| ||||||||||||
Db     616 ACTTCTTCGATGTCATGACTGGTAGATTTGGGGCCCCCGTATCAGGCGTGTATTTCTTCA 675

Qy     573 CCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATG 632
           |||||||||||||||||||||||| || ||||||||||||||||||||||||||||||||
Db     676 CCTTCAGCATGATGAAGCATGAGGACGTGGAGGAAGTGTATGTGTACCTTATGCACAATG 735

Qy     633 GCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCA 692
           | ||||| || ||||||||||||||||||||||  ||||| ||||||||||||||||||||
Db     736 GTAACACGGTGTTCAGCATGTACAGCTATGAAACAAAGGGAAAATCAGATACATCCAGCA 795
```

```
Qy     693 ATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCG 752
           | ||||| ||||||||| | |||||||| ||||| || |||||  |||||||||| || |
Db     796 ACCATGCAGTGCTGAAGTTGGCCAAAGGAGATGAAGTCTGGCTAAGAATGGGCAACGGTG 855

Qy     753 CTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTA 812
           | ||||||||||||||||| |||||||| ||||| ||||| || ||||| ||||||||||
Db     856 CCCTCCATGGGGACCACCAGCGCTTCTCTACCTTCGCAGGCTTTCTGCTTTTTGAAACTA 915

Qy     813 AGTAAATATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCT-GATTTG 871
           ||| |  |       || |||||||||   |  ||  || |||||| |||||| |  ||| 
Db     916 AGTGATGAGGAAGTCAGGATAGCTCCATGCTAAGGGCGATTTGTAGGTGAGCTAGGGTTG 975

Qy     872 TTACGATCTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATTATTG 931
           ||| |||||||||    ||  ||||| || || |  || |     || |       ||||
Db     976 TTAGGATCTGAGGGGTGTTGGAGTTG-GGCTTCTCTATGGAGTATTTAACTGTTACATTG 1034

Qy     932 GTTGCAATGTTGTTCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGA 991
           ||  || || |  |||  |||  || | |||||| |||||||| | || |||||||  ||
Db    1035 GTCACACTGCTACTCATTCTAATGGCATACCAATTATGTTGGATACTTTAGGGGCTAGGA 1094

Qy     992 AGAATCAACCACAAAATAGTCTTCTCAGA 1020
           |||||  |||||||  || | ||| ||||
Db    1095 AGAATAGACCACAAGGTAATATTCCCAGA 1123
```

RESULT 15
AAZ61730
ID  AAZ61730 standard; cDNA; 1123 BP.
XX
AC  AAZ61730;
XX
DT  27-MAR-2000  (first entry)
XX
DE  cDNA encoding rat skin cell secreted protein, SEQ ID NO:203.
XX
KW  Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast;
KW  embryonic skin cell; keratinocyte stem cell; transit amplifying cell;
KW  secreted; transmembrane; inflammation; cancer; neurological disease;
KW  angiogenesis; tumour vascularisation; growth disorder;
KW  developmental disorder; skin wound; hair follicle disorder;
KW  anti-inflammatory; cytostatic; neuroprotective; vulnery; ss.
XX
OS  Rattus sp.
XX
PN  WO9955865-A1.
XX
PD  04-NOV-1999.
XX
PF  29-APR-1999;  99WO-NZ00051.
XX
PR  29-APR-1998;  98US-0069726.
PR  09-NOV-1998;  98US-0188930.
XX
PA  (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI  Strachan L,  Sleeman M,  Watson JD,  Onrust R,  Kumble A,  Murison JG;
XX
DR  WPI; 2000-072177/06.
DR  P-PSDB; AAY76025.
XX
PT  Novel polynucleotides useful for the treatment of various conditions
PT  including wounds and cancer -
XX
PS  Claim 1; Page 137; 235pp; English.
XX
CC  The invention relates to novel nucleic acid sequences derived from rat
CC  dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,
CC  and mouse embryonic skin, keratinocyte stem cells and transit amplifying
CC  cells. Polypeptides of the invention may be used to treat inflammation,
CC  cancer and neurological diseases. The proteins may be used to stimulate
CC  the growth and motility of keratinocytes, to inhibit the growth of
CC  cancer cells, to modulate angiogenesis and tumour vascularisation, to
CC  modulate skin inflammation, to modulate epithelial cell growth and to
CC  inhibit binding of HIV-1 to leukocytes. The invention may also be used
CC  to treat growth and developmental defects, skin wounds and hair follicle
CC  disorders. Sequences AAZ61606-Z61832 represent cDNA sequences derived
CC  from several mouse, rat or human skin cell types. Sequences
CC  AAZ61606-Z61649, AAZ61725-Z61765, AAZ61802-Z61811 and AAZ61826 encode
CC  proteins with an N-terminal signal sequence, indicating that the proteins
CC  are secreted. Sequences AAZ61650-Z61668, AAZ61766-Z61780, AAZ61812-Z61817
CC  and AAZ61827-Z61829 encode proteins with one or more putative
CC  transmembrane domains.
XX
SQ  Sequence 1123 BP; 277 A; 266 C; 321 G; 258 T; 1 other;

Query Match  40.7%;  Score 696.2;  DB 21;  Length 1123;
Best Local Similarity  82.8%;  Pred. No. 5.3e-192;
Matches  819;  Conservative  0;  Mismatches  168;  Indels  2;  Gaps  2;

```
Qy      33 CTCTGCTGTCTTCTCAGGGAGACTCTGAGGCTCTGTTGAGAATCATGCTTTGGAGGCAGC 92
           | |  | |  | | | |||||| |||| | | |||  || ||||||  |||||||||
Db     136 CCCATCAGCTTCCCCGGGGAGATTCTGCCGATTTGTCACGAGCCATGCTCAGGAGGCAGC 195

Qy      93 TCATCTATTGGCAACTGCTGGCTTTGTTTTTCCTCCCTTTTTGCCTGTGTCAAGATGAAT 152
           || |||  ||||| |||||||||||| |||||||||| ||||||||||||||||||||||
Db     196 TCGTCTGGTGGCACCTGCTGGCTTTGCTTTTCCTCCCATTTTGCCTGTGTCAAGATGAAT 255

Qy     153 ACATGGAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAG 212
           |||||||||||||||| | |||||||| |||||||||||||| ||||||||-|||||||
Db     256 ACATGGAGTCTCCACAAGCTGGAGGACTGCCCCCAGACTGCAGCAAGTGTTGCCATGGAG 315

Qy     213 ACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAG 272
           | ||  | || || || |||||||| |||||||| || || || ||||||||||||||||
Db     316 ATTATGGATTCCGTGGTTACCAAGGGCCCCCTGGACCCCCAGGTCCTCCTGGCATTCCAG 375

Qy     273 GAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGA 332
           |||||||||||||||||| || || |||||||||| || ||||| ||||| |||||||
Db     376 GAAACCATGGAAACAATGGAAATAACGGAGCCACTGGCCACGAAGGGGCCAAGGGTGAGA 435

Qy     333 AGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAGCATGGCCCCAAAGGAG 392
           | || |||||||| |||||||||||||||||||| ||||||||||||||||||||||||
Db     436 AAGGAGACAAAGGCGACCTGGGGCCTCGAGGGGAACGGGGGCAGCATGGCCCCAAAGGAT 495

Qy     393 AGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAA 452
           ||||||| ||||| ||| | |||||||| || |||||||| |||||||||||||| || |
Db     496 AGAAGGGATACCCAGGGGTGCCACCAGAGCTGCAGATTGCGTTCATGGCTTCTCTAGCGA 555

Qy     453 CCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAA 512
           | |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     556 CTCACTTCAGCAATCAGAACAGTGGCATTATCTTCAGCAGTGTTGAGACCAACATTGGAA 615

Qy     513 ACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGGTGTGTATTTCTTCA 572
           ||||||| |||||||||||||||||||||||||||| |||||||| ||||||||||||||
Db     616 ACTTCTTCGATGTCATGACTGGTAGATTTGGGGCCCCCGTATCAGGCGTGTATTTCTTCA 675

Qy     573 CCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATG 632
           |||||||||||||||||||||||||| || ||||||||||||||||||||||||||||||
Db     676 CCTTCAGCATGATGAAGCATGAGGACGTGGAGGAAGTGTATGTGTACCTTATGCACAATG 735

Qy     633 GCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCA 692
           | ||||| || ||||||||||||||||||||||  ||||| ||||||||||||||||||
Db     736 GTAACACGGTGTTCAGCATGTACAGCTATGAAACAAAGGGAAAATCAGATACATCCAGCA 795

Qy     693 ATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCG 752
           | ||||| ||||||||| | |||||||| ||||| || |||||  |||||||||| || |
Db     796 ACCATGCAGTGCTGAAGTTGGCCAAAGGAGATGAAGTCTGGCTAAGAATGGGCAACGGTG 855

Qy     753 CTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTA 812
           | ||||||||||||||||| |||||||| ||||| ||||| || ||||| ||||||||||
Db     856 CCCTCCATGGGGACCACCAGCGCTTCTCTACCTTCGCAGGCTTTCTGCTTTTTGAAACTA 915

Qy     813 AGTAAATATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCT-GATTTG 871
           ||| |  |       || |||||||||   |  ||  || |||||| |||||| |  ||| 
Db     916 AGTGATGAGGAAGTCAGGATAGCTCCATGCTAAGGGCGATTTGTAGGTGAGCTAGGGTTG 975

Qy     872 TTACGATCTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATTATTG 931
```

```
          ||| |||||||||    ||  ||||| || || |  || |     || |       ||||
Db    976 TTAGGATCTGAGGGGTGTTGGAGTTG-GGCTTCTCTATGGAGTATTTAACTGTTACATTG 1034

Qy    932 GTTGCAATGTTGTTCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGA 991
          ||  || || |  |||  |||  || | |||||| |||||||| | || |||||||  ||
Db   1035 GTCACACTGCTACTCATTCTAATGGCATACCAATTATGTTGGATACTTTAGGGGCTAGGA 1094

Qy    992 AGAATCAACCACAAAATAGTCTTCTCAGA 1020
          |||||  |||||||  || | |||  ||||
Db   1095 AGAATAGACCACAAGGTAATATTCCCAGA 1123


RESULT 16
AAC99566
ID   AAC99566 standard; cDNA; 1123 BP.
XX
AC   AAC99566;
XX
DT   08-MAR-2001  (first entry)
XX
DE   Skin cell cDNA, SEQ ID NO: 28.
XX
KW   Rat; skin cell; cytostatic; antiinflammatory; anti-HIV;
KW   nootropic; neuroprotective; vulnerary; immunomodulatory; vaccine;
KW   keratinocyte growth stimulation; cancer; angiogenesis inhibition;
KW   inflammation; neurological disease; ss.
XX
OS   Rattus sp.
XX
PN   WO200069884-A2.
XX
PD   23-NOV-2000.
XX
PF   15-MAY-2000; 2000WO-NZ00075.
XX
PR   14-MAY-1999;   99US-0312283.
XX
PA   (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI   Watson JD,  Strachan L,  Onrust R,  Sleeman M,  Kumble KD,  Murison JG;
XX
DR   WPI; 2001-007495/01.
DR   P-PSDB; AAB55908.
XX
PT   New isolated polynucleotide used in the identification of genetic
PT   disorders and encoding polypeptides used for treating inflammatory
PT   disease, cancer and neurological diseases -
XX
PS   Claim 1; Page 87; 352pp; English.
XX
CC   The present polynucleotide encodes a polypeptide which is expressed in
CC   mammalian skin cells. The polypeptide is useful for stimulating
CC   keratinocyte growth and motility, inhibiting the growth of cancer cells,
CC   modulating angiogenesis, inhibiting angiogenesis and vascularisation of
CC   tumours, modulating skin inflammation, stimulating the growth of
CC   epithelial cells, inhibiting the binding of human immunodeficiency virus
CC   (HIV)-1 to leukocytes, and treating inflammmatory disease, cancer and
CC   neurological diseases. The polynucleotide can be used as a marker, in
CC   the identification of genetic disorders, and for the design of
CC   oligonucleotides for examining expression patterns.
XX
SQ   Sequence 1123 BP; 277 A; 266 C; 321 G; 258 T; 1 other;

  Query Match             40.7%;  Score 696.2;  DB 22;  Length 1123;
  Best Local Similarity   82.8%;  Pred. No. 5.3e-192;
  Matches  819;  Conservative    0;  Mismatches  168;  Indels    2;  Gaps    2;

Qy      33 CTCTGCTGTCTTCTCAGGGAGACTCTGAGGCTCTGTTGAGAATCATGCTTTGGAGGCAGC 92
           | |  | |  | | | |||||| ||||  | | |||   ||  ||||||  |||||||||
Db     136 CCCATCAGCTTCCCCGGGGAGATTCTGCCGATTTGTCACGAGCCATGCTCAGGAGGCAGC 195

Qy      93 TCATCTATTGGCAACTGCTGGCTTTGTTTTTCCTCCCTTTTTGCCTGTGTCAAGATGAAT 152
           || |||  ||||| |||||||||||| |||||||||| ||||||||||||||||||||||


Db    196 TCGTCTGGTGGCACCTGCTGGCTTTGCTTTTCCTCCCATTTTGCCTGTGTCAAGATGAAT 255

Qy    153 ACATGGAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAG 212
          |||||||||||||||| | |||||||| |||||||||||| ||||||| |||||||
Db    256 ACATGGAGTCTCCACAAGCTGGAGGACTGCCCCCAGACTGCAGCAAGTGTTGCCATGGAG 315

Qy    213 ACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAG 272
          | ||  | || || || |||||||| |||||||| || || || ||||||||||||||||
Db    316 ATTATGGATTCCGTGGTTACCAAGGGCCCCCTGGACCCCCAGGTCCTCCTGGCATTCCAG 375

Qy    273 GAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGA 332
          |||||||||||||||||| || || |||||||||| || ||||| ||||| |||||||
Db    376 GAAACCATGGAAACAATGGAAATAACGGAGCCACTGGCCACGAAGGGGCCAAGGGTGAGA 435

Qy    333 AGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAGCATGGCCCCAAAGGAG 392
          | || |||||||| |||||||||||||||||||| ||||||||||||||||||||||||
Db    436 AAGGAGACAAAGGCGACCTGGGGCCTCGAGGGGAACGGGGGCAGCATGGCCCCAAAGGAT 495

Qy    393 AGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAA 452
          ||||||| ||||| ||| | |||||||| || |||||||| |||||||||||||| || |
Db    496 AGAAGGGATACCCAGGGGTGCCACCAGAGCTGCAGATTGCGTTCATGGCTTCTCTAGCGA 555

Qy    453 CCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAA 512
          | |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    556 CTCACTTCAGCAATCAGAACAGTGGCATTATCTTCAGCAGTGTTGAGACCAACATTGGAA 615

Qy    513 ACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGGTGTGTATTTCTTCA 572
          ||||||| |||||||||||||||||||||||||||| |||||||| ||||||||||||
Db    616 ACTTCTTCGATGTCATGACTGGTAGATTTGGGGCCCCCGTATCAGGCGTGTATTTCTTCA 675

Qy    573 CCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATG 632
          |||||||||||||||||||||||| || ||||||||||||||||||||||||||||||||
Db    676 CCTTCAGCATGATGAAGCATGAGGACGTGGAGGAAGTGTATGTGTACCTTATGCACAATG 735

Qy    633 GCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCA 692
          | ||||| || |||||||||||||||||||||  ||||| ||||||||||||||||||||
Db    736 GTAACACGGTGTTCAGCATGTACAGCTATGAAACAAAGGGAAAATCAGATACATCCAGCA 795

Qy    693 ATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCG 752
          | ||||| |||||||||| | |||||||| ||||| || |||||  |||||||||| || |
Db    796 ACCATGCAGTGCTGAAGTTGGCCAAAGGAGATGAAGTCTGGCTAAGAATGGGCAACGGTG 855

Qy    753 CTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTA 812
          | |||||||||||||||| |||||||| ||||| ||||| || |||||  ||||||||||
Db    856 CCCTCCATGGGGACCACCAGCGCTTCTCTACCTTCGCAGGCTTTCTGCTTTTTGAAACTA 915

Qy    813 AGTAAATATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCT-GATTTG 871
          ||| |  |       || |||||||||   |  ||  || |||||| ||||||  |  |||
Db    916 AGTGATGAGGAAGTCAGGATAGCTCCATGCTAAGGGCGATTTGTAGGTGAGCTAGGGTTG 975

Qy    872 TTACGATCTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATTATTG 931
          ||| |||||||||    ||  ||||| || || |  || |     || |       ||||
Db    976 TTAGGATCTGAGGGGTGTTGGAGTTG-GGCTTCTCTATGGAGTATTTAACTGTTACATTG 1034

Qy    932 GTTGCAATGTTGTTCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGA 991
          ||  || || |  |||  |||  || | |||||| |||||||| | || |||||||  ||
Db   1035 GTCACACTGCTACTCATTCTAATGGCATACCAATTATGTTGGATACTTTAGGGGCTAGGA 1094

Qy    992 AGAATCAACCACAAAATAGTCTTCTCAGA 1020
          |||||  |||||||  || | |||  ||||
Db   1095 AGAATAGACCACAAGGTAATATTCCCAGA 1123


RESULT 17
AAC99663
ID   AAC99663 standard; cDNA; 1123 BP.
XX
AC   AAC99663;
XX
DT   08-MAR-2001  (first entry)
XX
DE   Skin cell cDNA, SEQ ID NO: 203.
XX
```

```
KW   Rat; skin cell; cytostatic; antiinflammatory; anti-HIV;
KW   nootropic; neuroprotective; vulnerary; immunomodulatory; vaccine;
KW   keratinocyte growth stimulation; cancer; angiogenesis inhibition;
KW   inflammation; neurological disease; ss.
XX
OS   Rattus sp.
XX
PN   WO200069884-A2.
XX
PD   23-NOV-2000.
XX
PF   15-MAY-2000; 2000WO-NZ00075.
XX
PR   14-MAY-1999;   99US-0312283.
XX
PA   (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI   Watson JD,  Strachan L,  Onrust R,  Sleeman M,  Kumble KD,  Murison JG;
XX
DR   WPI; 2001-007495/01.
DR   P-PSDB; AAB55958.
XX
PT   New isolated polynucleotide used in the identification of genetic
PT   disorders and encoding polypeptides used for treating inflammatory
PT   disease, cancer and neurological diseases -
XX
PS   Claim 1; Page 176-177; 352pp; English.
XX
CC   The present polynucleotide encodes a polypeptide which is expressed in
CC   mammalian skin cells. The polypeptide is useful for stimulating
CC   keratinocyte growth and motility, inhibiting the growth of cancer cells,
CC   modulating angiogenesis, inhibiting angiogenesis and vascularisation of
CC   tumours, modulating skin inflammation, stimulating the growth of
CC   epithelial cells, inhibiting the binding of human immunodeficiency virus
CC   (HIV)-1 to leukocytes, and treating inflammmatory disease, cancer and
CC   neurological diseases. The polynucleotide can be used as a marker, in
CC   the identification of genetic disorders, and for the design of
CC   oligonucleotides for examining expression patterns.
XX
SQ   Sequence 1123 BP; 277 A; 266 C; 321 G; 258 T; 1 other;

  Query Match             40.7%;  Score 696.2;  DB 22;  Length 1123;
  Best Local Similarity   82.8%;  Pred. No. 5.3e-192;
  Matches  819;  Conservative    0;  Mismatches  168;  Indels    2;  Gaps    2;

Qy      33 CTCTGCTGTCTTCTCAGGGAGACTCTGAGGCTCTGTTGAGAATCATGCTTTGGAGGCAGC 92
           | |  | |  | | | |||||| ||||  | | |||   ||  ||||||  |||||||||
Db     136 CCCATCAGCTTCCCCGGGGAGATTCTGCCGATTTGTCACGAGCCATGCTCAGGAGGCAGC 195

Qy      93 TCATCTATTGGCAACTGCTGGCTTTGTTTTTCCTCCCTTTTTGCCTGTGTCAAGATGAAT 152
           || |||  ||||| |||||||||||| |||||||||| ||||||||||||||||||||||
Db     196 TCGTCTGGTGGCACCTGCTGGCTTTGCTTTTCCTCCCATTTTGCCTGTGTCAAGATGAAT 255

Qy     153 ACATGGAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAG 212
           |||||||||||||||| | |||||||| |||||||||||||| |||||||| |||||||
Db     256 ACATGGAGTCTCCACAAGCTGGAGGACTGCCCCCAGACTGCAGCAAGTGTTGCCATGGAG 315

Qy     213 ACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAG 272
           | ||  | || || || |||||||| |||||||| || || || ||||||||||||||||
Db     316 ATTATGGATTCCGTGGTTACCAAGGGCCCCCTGGACCCCCAGGTCCTCCTGGCATTCCAG 375

Qy     273 GAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGA 332
           |||||||||||||||||| || || |||||||||| || ||||| ||||| |||||||
Db     376 GAAACCATGGAAACAATGGAAATAACGGAGCCACTGGCCACGAAGGGGCCAAGGGTGAGA 435

Qy     333 AGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAGCATGGCCCCAAAGGAG 392
           | || |||||||| |||||||||||||||||| ||||||||||||||||||||||||||
Db     436 AAGGAGACAAAGGCGACCTGGGGCCTCGAGGGGAACGGGGGCAGCATGGCCCCAAAGGAT 495

Qy     393 AGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAA 452
           ||||||| ||||| ||| | |||||||| || |||||||| |||||||||||||| || |
Db     496 AGAAGGGATACCCAGGGGTGCCACCAGAGCTGCAGATTGCGTTCATGGCTTCTCTAGCGA 555

Qy     453 CCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAA 512
           | |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db     556 CTCACTTCAGCAATCAGAACAGTGGCATTATCTTCAGCAGTGTTGAGACCAACATTGGAA 615

Qy     513 ACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGGTGTGTATTTCTTCA 572
           ||||||| |||||||||||||||||||||||||||| |||||||| ||||||||||||
Db     616 ACTTCTTCGATGTCATGACTGGTAGATTTGGGGCCCCCGTATCAGGCGTGTATTTCTTCA 675

Qy     573 CCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATG 632
           |||||||||||||||||||||||||| || ||||||||||||||||||||||||||||||
Db     676 CCTTCAGCATGATGAAGCATGAGGACGTGGAGGAAGTGTATGTGTACCTTATGCACAATG 735

Qy     633 GCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCA 692
           | ||||| || |||||||||||||||||||||  ||||| ||||||||||||||||||||
Db     736 GTAACACGGTGTTCAGCATGTACAGCTATGAAACAAAGGGAAAATCAGATACATCCAGCA 795

Qy     693 ATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCG 752
           | ||||| ||||||||| | |||||||| ||||| || |||||  |||||||||| || |
Db     796 ACCATGCAGTGCTGAAGTTGGCCAAAGGAGATGAAGTCTGGCTAAGAATGGGCAACGGTG 855

Qy     753 CTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTA 812
           | |||||||||||||||| |||||||| |||||  ||||| || |||||  ||||||||||
Db     856 CCCTCCATGGGGACCACCAGCGCTTCTCTACCTTCGCAGGCTTTCTGCTTTTTGAAACTA 915

Qy     813 AGTAAATATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCT-GATTTG 871
           ||| |  |       || |||||||||   |  ||  || |||||| ||||||  |  |||
Db     916 AGTGATGAGGAAGTCAGGATAGCTCCATGCTAAGGGCGATTTGTAGGTGAGCTAGGGTTG 975

Qy     872 TTACGATCTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATTATTG 931
           ||| |||||||||     ||  ||||| || || |  || |     || |       ||||
Db     976 TTAGGATCTGAGGGGTGTTGGAGTTG-GGCTTCTCTATGGAGTATTTAACTGTTACATTG 1034

Qy     932 GTTGCAATGTTGTTCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGA 991
           ||  || || |  |||  |||  || | |||||| |||||||| | || |||||||  ||
Db    1035 GTCACACTGCTACTCATTCTAATGGCATACCAATTATGTTGGATACTTTAGGGGCTAGGA 1094

Qy     992 AGAATCAACCACAAAATAGTCTTCTCAGA 1020
           |||||  |||||||  || | ||| ||||
Db    1095 AGAATAGACCACAAGGTAATATTCCCAGA 1123


RESULT 18
ABL34718
ID   ABL34718 standard; cDNA; 1123 BP.
XX
AC   ABL34718;
XX
DT   04-APR-2002  (first entry)
XX
DE   Rat cDNA isolated from skin cells SEQ ID NO: 28.
XX
KW   Human; rat; mouse; skin cell; skin wound; cancer; growth defect;
KW   developmental defect; inflammatory disease; dermatological; vulnerary;
KW   immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene;
KW   ss.
XX
OS   Rattus sp.
XX
PN   WO200190357-A1.
XX
PD   29-NOV-2001.
XX
PF   24-MAY-2001; 2001WO-NZ00099.
XX
PR   24-MAY-2000; 2000US-206650P.
PR   25-JUL-2000; 2000US-221232P.
XX
PA   (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI   Watson JD,  Strachan L,  Sleeman M,  Onrust R,  Murison JG,  Kumble KD;
XX
DR   WPI; 2002-122020/16.
XX
```

PT New polynucleotides and polypeptides encoded by the polynucleotides
PT isolated from skin cells, useful for treating skin wounds, cancers,
PT growth and developmental defects, inflammatory diseases, or for
PT modulating immune responses -
XX
PS Claim 1; Page 86-87; 466pp; English.
XX
CC The present invention provides the protein and coding sequences of cDNAs
CC isolated from human, murine and rat skin cell libraries. The sequences
CC can be used in the development of therapeutic agents useful in the
CC treatment of skin diseases, including skin wounds, cancer, growth
CC defects, developmental defects and inflammatory diseases. The proteins
CC have important roles in the induction of hair growth, cell proliferation
CC and cell-cell interaction, in maintaining tissue integrity, in wound
CC healing and in modulating immune responses. The present sequence is a
CC cDNA of the invention.
XX
SQ Sequence 1123 BP; 277 A; 266 C; 321 G; 258 T; 1 other;

Query Match 40.7%; Score 696.2; DB 24; Length 1123;
Best Local Similarity 82.8%; Pred. No. 5.3e-192;
Matches 819; Conservative 0; Mismatches 168; Indels 2; Gaps 2;

```
Qy      33 CTCTGCTGTCTTCTCAGGGAGACTCTGAGGCTCTGTTGAGAATCATGCTTTGGAGGCAGC 92
           | |  | |  | | | |||||| ||||  | | |||   ||  ||||||  |||||||||
Db     136 CCCATCAGCTTCCCCGGGGAGATTCTGCCGATTTGTCACGAGCCATGCTCAGGAGGCAGC 195

Qy      93 TCATCTATTGGCAACTGCTGGCTTTGTTTTCCTCCCTTTTTGCCTGTGTCAAGATGAAT 152
           || |||  ||||| ||||||||||||| |||||||||| ||||||||||||||||||||||
Db     196 TCGTCTGGTGGCACCTGCTGGCTTTGCTTTTCCTCCCATTTTGCCTGTGTCAAGATGAAT 255

Qy     153 ACATGGAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAG 212
           |||||||||||||||| | |||||||| |||||||||||||| |||||||| |||||||
Db     256 ACATGGAGTCTCCACAAGCTGGAGGACTGCCCCCAGACTGCAGCAAGTGTTGCCATGGAG 315

Qy     213 ACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAG 272
           | ||  | || || || |||||||| |||||||| || || || ||||||||||||||||
Db     316 ATTATGGATTCCGTGGTTACCAAGGGCCCCCTGGACCCCCAGGTCCTCCTGGCATTCCAG 375

Qy     273 GAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGA 332
           |||||||||||||||||| || || |||||||||| || ||||| ||||| |||||||
Db     376 GAAACCATGGAAACAATGGAAATAACGGAGCCACTGGCCACGAAGGGGCCAAGGGTGAGA 435

Qy     333 AGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAGCATGGCCCCAAAGGAG 392
           | || |||||||| |||||||||||||||||||| ||||||||||||||||||||||||
Db     436 AAGGAGACAAAGGCGACCTGGGGCCTCGAGGGGAACGGGGGCAGCATGGCCCCAAAGGAT 495

Qy     393 AGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAA 452
           ||||||| ||||| ||| | |||||||| || |||||||| |||||||||||||| || |
Db     496 AGAAGGGATACCCAGGGGTGCCACCAGAGCTGCAGATTGCGTTCATGGCTTCTCTAGCGA 555

Qy     453 CCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAA 512
           | |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     556 CTCACTTCAGCAATCAGAACAGTGGCATTATCTTCAGCAGTGTTGAGACCAACATTGGAA 615

Qy     513 ACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGGTGTGTATTTCTTCA 572
           ||||||| |||||||||||||||||||||||||||||| |||||||| ||||||||||||
Db     616 ACTTCTTCGATGTCATGACTGGTAGATTTGGGGCCCCCGTATCAGGCGTGTATTTCTTCA 675

Qy     573 CCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATG 632
           |||||||||||||||||||||||| || ||||||||||||||||||||||||||||||||
Db     676 CCTTCAGCATGATGAAGCATGAGGACGTGGAGGAAGTGTATGTGTACCTTATGCACAATG 735

Qy     633 GCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCA 692
           | ||||| || |||||||||||||||||||||  ||||| ||||||||||||||||||||
Db     736 GTAACACGGTGTTCAGCATGTACAGCTATGAAACAAAGGGAAAATCAGATACATCCAGCA 795

Qy     693 ATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCG 752
           | ||||| ||||||||| | |||||||| ||||| || |||||  |||||||||| || |
Db     796 ACCATGCAGTGCTGAAGTTGGCCAAAGGAGATGAAGTCTGGCTAAGAATGGGCAACGGTG 855

Qy     753 CTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTA 812
           | |||||||||||||||| |||||||| ||||| ||||| || ||||| ||||||||||
Db     856 CCCTCCATGGGGACCACCAGCGCTTCTCTACCTTCGCAGGCTTTCTGCTTTTTGAAACTA 915

Qy     813 AGTAAATATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCT-GATTTG 871
           ||| |  |       || |||||||||   |  ||  || |||||| |||||| |  |||
Db     916 AGTGATGAGGAAGTCAGGATAGCTCCATGCTAAGGGCGATTTGTAGGTGAGCTAGGGTTG 975

Qy     872 TTACGATCTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATTATTG 931
           ||| |||||||||    ||  ||||| || || |  || |     || |       ||||
Db     976 TTAGGATCTGAGGGGTGTTGGAGTTG-GGCTTCTCTATGGAGTATTTAACTGTTACATTG 1034

Qy     932 GTTGCAATGTTGTTCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGA 991
           ||  || || |  |||  |||  || | |||||| |||||||| | || |||||||  ||
Db    1035 GTCACACTGCTACTCATTCTAATGGCATACCAATTATGTTGGATACTTTAGGGGCTAGGA 1094

Qy     992 AGAATCAACCACAAAATAGTCTTCTCAGA 1020
           |||||  |||||||  || | ||| ||||
Db    1095 AGAATAGACCACAAGGTAATATTCCCAGA 1123
```

RESULT 19
ABL34815
ID ABL34815 standard; cDNA; 1123 BP.
XX
AC ABL34815;
XX
DT 04-APR-2002 (first entry)
XX
DE Rat cDNA isolated from skin cells SEQ ID NO: 203.
XX
KW Human; rat; mouse; skin cell; skin wound; cancer; growth defect;
KW developmental defect; inflammatory disease; dermatological; vulnerary;
KW immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene;
KW ss.
XX
OS Rattus sp.
XX
PN WO200190357-A1.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-NZ00099.
XX
PR 24-MAY-2000; 2000US-206650P.
PR 25-JUL-2000; 2000US-221232P.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG, Kumble KD;
XX
DR WPI; 2002-122020/16.
XX
PT New polynucleotides and polypeptides encoded by the polynucleotides
PT isolated from skin cells, useful for treating skin wounds, cancers,
PT growth and developmental defects, inflammatory diseases, or for
PT modulating immune responses -
XX
PS Claim 1; Page 155-156; 466pp; English.
XX
CC The present invention provides the protein and coding sequences of cDNAs
CC isolated from human, murine and rat skin cell libraries. The sequences
CC can be used in the development of therapeutic agents useful in the
CC treatment of skin diseases, including skin wounds, cancer, growth
CC defects, developmental defects and inflammatory diseases. The proteins
CC have important roles in the induction of hair growth, cell proliferation
CC and cell-cell interaction, in maintaining tissue integrity, in wound
CC healing and in modulating immune responses. The present sequence is a
CC cDNA of the invention.
XX
SQ Sequence 1123 BP; 277 A; 266 C; 321 G; 258 T; 1 other;

Query Match 40.7%; Score 696.2; DB 24; Length 1123;
Best Local Similarity 82.8%; Pred. No. 5.3e-192;
Matches 819; Conservative 0; Mismatches 168; Indels 2; Gaps 2;

```
Qy      33 CTCTGCTGTCTTCTCAGGGAGACTCTGAGGCTCTGTTGAGAATCATGCTTTGGAGGCAGC 92
           | |  | |  | | | |||||| ||||  | | |||   ||  ||||||  |||||||||
Db     136 CCCATCAGCTTCCCCGGGGAGATTCTGCCGATTTGTCACGAGCCATGCTCAGGAGGCAGC 195

Qy      93 TCATCTATTGGCAACTGCTGGCTTTGTTTTTCCTCCCTTTTTGCCTGTGTCAAGATGAAT 152
           || |||  ||||| |||||||||||| |||||||||| ||||||||||||||||||||||
Db     196 TCGTCTGGTGGCACCTGCTGGCTTTGCTTTTCCTCCCATTTTGCCTGTGTCAAGATGAAT 255

Qy     153 ACATGGAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAG 212
           ||||||||||||||||| | |||||||| |||||||||||||| |||||||| |||||||.
Db     256 ACATGGAGTCTCCACAAGCTGGAGGACTGCCCCCAGACTGCAGCAAGTGTTGCCATGGAG 315

Qy     213 ACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAG 272
           | ||  | || || || |||||||| |||||||| || || || ||||||||||||||||
Db     316 ATTATGGATTCCGTGGTTACCAAGGGCCCCCTGGACCCCCAGGTCCTCCTGGCATTCCAG 375

Qy     273 GAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGA 332
           |||||||||||||||| || || |||||||||| || ||||| ||||| |||||||
Db     376 GAAACCATGGAAACAATGGAAATAACGGAGCCACTGGCCACGAAGGGGCCAAGGGTGAGA 435

Qy     333 AGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAGCATGGCCCCAAAGGAG 392
           | || |||||||| |||||||||||||||||||| |||||||||||||||||||||||||
Db     436 AAGGAGACAAAGGCGACCTGGGGCCTCGAGGGGAACGGGGGCAGCATGGCCCCAAAGGAT 495

Qy     393 AGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAA 452
           ||||||| ||||| ||| | |||||||| || |||||||| |||||||||||||| || |
Db     496 AGAAGGGATACCCAGGGGTGCCACCAGAGCTGCAGATTGCGTTCATGGCTTCTCTAGCGA 555

Qy     453 CCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAA 512
           | |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     556 CTCACTTCAGCAATCAGAACAGTGGCATTATCTTCAGCAGTGTTGAGACCAACATTGGAA 615

Qy     513 ACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGGTGTGTATTTCTTCA 572
           ||||||| |||||||||||||||||||||||||||| |||||||| ||||||||||||
Db     616 ACTTCTTCGATGTCATGACTGGTAGATTTGGGGCCCCCGTATCAGGCGTGTATTTCTTCA 675

Qy     573 CCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATG 632
           |||||||||||||||||||||||| || ||||||||||||||||||||||||||||||||
Db     676 CCTTCAGCATGATGAAGCATGAGGACGTGGAGGAAGTGTATGTGTACCTTATGCACAATG 735

Qy     633 GCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCA 692
           | ||||| || |||||||||||||||||||| ||||| |||||||||||||||||||||
Db     736 GTAACACGGTGTTCAGCATGTACAGCTATGAAACAAAGGGAAAATCAGATACATCCAGCA 795

Qy     693 ATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCG 752
           | ||||| |||||||| | |||||||| |||| || |||||  |||||||||| || |
Db     796 ACCATGCAGTGCTGAAGTTGGCCAAAGGAGATGAAGTCTGGCTAAGAATGGGCAACGGTG 855

Qy     753 CTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTA 812
           | |||||||||||||||| |||||||| |||| ||||| || |||| ||||||||||
Db     856 CCCTCCATGGGGACCACCAGCGCTTCTCTACCTTCGCAGGCTTTCTGCTTTTTGAAACTA 915

Qy     813 AGTAAATATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCT-GATTTG 871
           ||| |  |       || |||||||||   |  ||  || |||||| ||||||  |  |||
Db     916 AGTGATGAGGAAGTCAGGATAGCTCCATGCTAAGGGCGATTTGTAGGTGAGCTAGGGTTG 975

Qy     872 TTACGATCTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATTATTG 931
           ||| |||||||||    ||  |||||| || || |  || |     || |       ||||
Db     976 TTAGGATCTGAGGGGTGTTGGAGTTG-GGCTTCTCTATGGAGTATTTAACTGTTACATTG 1034

Qy     932 GTTGCAATGTTGTTCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGA 991
           ||  || || |  |||  |||  || | |||||| |||||||| | || |||||||  ||
Db    1035 GTCACACTGCTACTCATTCTAATGGCATACCAATTATGTTGGATACTTTAGGGGCTAGGA 1094

Qy     992 AGAATCAACCACAAAATAGTCTTCTCAGA 1020
           |||||  |||||||  || | ||| ||||
Db    1095 AGAATAGACCACAAGGTAATATTCCCAGA 1123
```

RESULT 20
AAC64064
ID AAC64064 standard; DNA; 1117 BP.

XX
AC AAC64064;
XX
DT 19-FEB-2001 (first entry)
XX
DE Mouse zacrp2 DNA, SEQ ID NO:11.
XX
KW Mouse zacrp2; adipocyte complement related protein homologue;
KW ACRP30; C1q domain; collagen-like domain; energy balance modulation;
KW cellular metabolism; metabolic disorder; obesity; anorexia;
KW antimicrobial agent; infection; platelet aggregation inhibition;
KW adhesion; activation; vascular injury; antibacterial; antiviral;
KW human zacrp3 homologue; ds.
XX
OS Mus musculus.
XX
PN WO200063377-A1.
XX
PD 26-OCT-2000.
XX
PF 19-APR-2000; 2000WO-US10454.
XX
PR 20-APR-1999; 99US-0294943.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Piddington CS, Bishop PD;
XX
DR WPI; 2000-665243/64.
DR P-PSDB; AAB29582.
XX
PT Novel zacrp3 polypeptides used to treat or prevent bacterial or viral
PT infections, for wound healing, improving blood flow, and to analyze
PT energy efficiency in mammals -
XX
PS Disclosure; Page 115-117; 123pp; English.
XX
CC The invention relates to the human zacrp3 protein (AAB29580) and to
CC nucleic acids which encode it (AAC64058, AAC64063). Zacrp3 is a homogue
CC of adipocyte complement related protein (ACRP30) and contains a
CC collagen-like domain comprising Gly-Xaa-Xaa or Gly-Xaa-Pro repeats, and a
CC C-terminal C1q domain comprising 10 beta-strands. The zacrp3 gene is
CC located on chromosome 5p12. The invention also relates to zacrp3
CC fragments, fusion proteins containing zacrp3 polypeptides,
CC zacrp3-specific antibodies, expression constructs and host cells
CC comprising zacrp3 nucleic acids, and methods of recombinant production of
CC zacrp3. Human zacrp3, and its agonists and antagonists may be used in the
CC study and modulation of cellular metabolism and energy balance in
CC mammals, and may therefore be used to treat disorders such as obesity and
CC anorexia, and conditions associated with these disorders. Due to its C1q
CC like domain, zacrp3 and zacrp3-containing fusion proteins may be useful
CC as antimicrobial agents, promoting lysis or phagocytosis of infectious
CC organisms such as bacteria or viruses. Zacrp3, its fragments, fusion
CC proteins, antibodies and activity modulators may also be used to inhibit
CC collagen-induced platelet aggregation, adhesion, or activation, and may
CC therefore have potential for promoting blood flow within the vasculature
CC of a mammal e.g., to treat injury to the vasculature or other collagenous
CC tissue. Human zacrp3 and its antibodies may additionally be used to study
CC dimerisation and oligomerisation. The present sequence represents DNA
CC encoding mouse zacrp2, a homologue of human zacrp3.
XX
SQ Sequence 1117 BP; 284 A; 272 C; 293 G; 268 T; 0 other;

Query Match 40.6%; Score 695.8; DB 21; Length 1117;
Best Local Similarity 85.5%; Pred. No. 6.9e-192;
Matches 786; Conservative 0; Mismatches 132; Indels 1; Gaps 1;

```
Qy      72 GAATCATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTCCTCCCTT 131
           ||  ||||||  |||||||| |||||  ||||| |||||| ||||| |||||||||| |
Db     106 GAGCCATGCTCGGGAGGCAGCGCATCTGGTGGCACCTGCTGCCTTTGCTTTTCCTCCCAT 165

Qy     132 TTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCCAGACT 191
           |||||||||||||||||||||||||||||||||||||||| | |||||||| ||||||||||
```

```
Db    166 TTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAGCTGGAGGACTGCCCCCAGACT 225

Qy    192 GCAGTAAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCAC 251
          |||| |||||||| |||||||| ||  | ||||| || |||||||| |||||||| || |
Db    226 GCAGCAAGTGTTGCCATGGAGATTATGGATTTCGTGGTTACCAAGGGCCCCCTGGACCTC 285

Qy    252 CGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTC 311
          | || ||||||||||||||||||||||||||||||||||| |||||||||| ||||| |
Db    286 CAGGTCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGGAACAATGGAGCTACTGGCC 345

Qy    312 ATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGG 371
          ||||||| |||||||||||||| || |||||||| ||||| || |||||||| || ||||
Db    346 ATGAAGGGGCCAAAGGTGAGAAAGGAGACAAAGGCGACCTAGGCCCTCGAGGAGAACGGG 405

Qy    372 GGCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTG 431
          |||||||||||||||||||||||||| |||||||| ||| | ||||||||||| |||||||
Db    406 GGCAGCATGGCCCCAAAGGAGAGAAAGGCTACCCAGGGGTGCCACCAGAACTGCAGATTG 465

Qy    432 CATTCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCA 491
          .  |||||||||||||||| ||||| |||||||||||||||||||||| ||||||||||||
Db    466 CATTCATGGCTTCTCTAGCAACTCACTTCAGCAATCAGAACAGTGGCATTATCTTCAGCA 525

Qy    492 GTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAG 551
          |||||||||||||||||||||||||| |||||||||||| |||||||||||||| |
Db    526 GTGTTGAGACCAACATTGGAAACTTCTTCGATGTCATGACTGGGAGATTTGGGGCCCCCG 585

Qy    552 TATCAGGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGT 611
          |||||||||||||||||||||||||||||||||||||||||||||||| ||| ||||||||||
Db    586 TATCAGGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGACGTAGAGGAAGTGT 645

Qy    612 ATGTGTACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGG 671
          |||||||||||||||||| |||||||||||||||||||||||||||||  ||||
Db    646 ATGTGTACCTTATGCACAACGGCAACACAGTCTTCAGCATGTACAGCTATGAAACAAAGG 705

Qy    672 GCAAATCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTT 731
          | |||||||||||||||||| ||||| |||||||| | |||||||| ||||| || |
Db    706 GAAAATCAGATACATCCAGCAACCATGCAGTGCTGAAGTTGGCCAAAGGAGATGAAGTCT 765

Qy    732 GGCTGCGAATGGGCAATGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAG 791
          ||||  |||||||||| || || ||||| |||||||||| |||||||||||||| ||||
Db    766 GGCTAAGAATGGGCAACGGTGCCCTCCACGGGGACCACCAGCGCTTCTCCACCTTCGCAG 825

Qy    792 GATTCCTGCTCTTTGAAACTAAGTAAATATATGACTAGAATAGCTCCACTTTGGGGAAGA 851
          | || ||||||||||||||||||| |  |        || ||| ||||||||||||||   |
Db    826 GCTTTCTGCTCTTTGAAACTAAGTGACAAGGAAGACAGGATATCTCCACTTTGGGGGCAA 885

Qy    852 CTTGTAGCTGAGCT-GATTTGTTACGATCTGAGGAACATTAAAGTTGAGGGTTTTACATT 910
           || |||||||||| |  |||||| ||| ||| | |  || |||| | ||||| |  ||
Db    886 TTTATAGCTGAGCTAGGGTTGTTAGGATATGAAGGATGTTGAAGTCGGGGGTTCTTTATG 945

Qy    911 GCTGTATTCAAAAAATTATTGGTTGCAATGTTGTTCACGCTACAGGTACACCAATAATGT 970
          |     || |       ||||||  || || |  |||  |||  || | ||||||||||
Db    946 GAGCATTTAAGTGTTGCATTGGTCACACTGCTACTCATTCTAATGGCATACCAATAATGT 1005

Qy    971 TGGACAATTCAGGGGCTCA 989
          ||||   ||||||||||||
Db   1006 TGGATGCTTCAGGGGCTCA 1024


RESULT 21
ABK35590
ID   ABK35590 standard; DNA; 960 BP.
XX
AC . ABK35590;
XX
DT   08-MAY-2002  (first entry)
XX
DE   Gene encoding novel human secreted or membrane-associated protein #9.
XX
KW   Human; secreted protein; membrane-associated protein; hypertension;
KW   inflammatory disorder; neurological disorder; haematopoietic disorder;
KW   skeletal developmental disorder; growth abnormality; autoimmune disorder;
KW   neurodegenerative disorder; nervous system disorder; bacterial infection;
KW   peripheral myelinopathy; viral infection; cancer; obesity; diabetes;
KW   hypotension; sexual development disorder; blood disorder; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200204600-A2.
XX
PD   17-JAN-2002.
XX
PF   12-JUL-2001; 2001WO-US21985.
XX
PR   12-JUL-2000; 2000US-218033P.
PR   21-AUG-2000; 2000US-226517P.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
PA   (GLAX ) GLAXO GROUP LTD.
XX
PI   Agarwal P,  Cogswell JP,  Lai Y,  Martensen SA,  Rizvi SK,  Strum JC;
PI   Smith RF,  Xiang Z,  Xie Q;
XX
DR   WPI; 2002-188468/24.
DR   P-PSDB; AAU84370.
XX
PT   Novel secreted and membrane-associated polypeptides and polynucleotides
PT   encoding the polypeptides, for preventing, treating and ameliorating
PT   cancers, mental or sexual developmental disorders, and malignant tumours
PT   -
XX
PS   Claim 2; Page 106; 151pp; English.
XX
CC   The present invention relates to the isolation of novel human secreted
CC   or membrane-associated proteins and the genes encoding them. The
CC   sequences of the invention are useful for treating, preventing and
CC   ameliorating various diseases such as inflammatory disorders (e.g.
CC   asthma), neurological disorders (e.g. dementia), haematopoietic
CC   disorders, skeletal developmental disorders, growth abnormalities,
CC   neurodegenerative disorders (e.g. Huntington's disease), nervous system
CC   disorders, autoimmune disorders (e.g. rheumatoid arthritis),
CC   peripheral myelinopathies, viral and bacterial infections,
CC   alpha-mannosidosis, diabetes, cancers, malignant tumours, hyper- and
CC   hypotension, obesity, bulimia, anorexia, manic depression, delirium,
CC   mental retardation, Tourette's syndrome, schizophrenia, growth, mental
CC   or sexual development disorders, and dysfunctions of the blood cascade
CC   system including those leading to stroke. ABK35582-ABK35609 represent
CC   the genes encoding the novel human secreted or membrane-associated
CC   proteins of the invention.
XX
SQ   Sequence 960 BP; 261 A; 232 C; 262 G; 205 T; 0 other;

  Query Match             38.5%;  Score 659;  DB 24;  Length 960;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-181;
  Matches  659;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    159 AGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTACA 218
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    302 AGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTACA 361

Qy    219 GCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACC 278
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    362 GCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACC 421

Qy    279 ATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCG 338
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    422 ATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCG 481

Qy    339 ACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAGG 398
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    482 ACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAGG 541

Qy    399 GCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCACT 458
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    542 GCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCACT 601
```

```
Qy     459 TCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTCT 518
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     602 TCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTCT 661

Qy     519 TTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGGTGTGTATTTCTTCACCTTCA 578
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     662 TTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGGTGTGTATTTCTTCACCTTCA 721

Qy     579 GCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATGGCAACA 638
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     722 GCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATGGCAACA 781

Qy     639 CAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCAATCATG 698
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     782 CAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCAATCATG 841

Qy     699 CTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTCC 758
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     842 CTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTCC 901

Qy     759 ATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTAAGTAA 817
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     902 ATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTAAGTAA 960
```

RESULT 22
AAC64063
ID AAC64063 standard; DNA; 738 BP.
XX
AC AAC64063;
XX
DT 19-FEB-2001 (first entry)
XX
DE Human zacrp3 degenerate DNA, SEQ ID NO:10.
XX
KW Human zacrp3; adipocyte complement related protein homologue;
KW ACRP30; C1q domain; collagen-like domain; energy balance modulation;
KW cellular metabolism; metabolic disorder; obesity; anorexia;
KW antimicrobial agent; infection; platelet aggregation inhibition;
KW adhesion; activation; vascular injury; antibacterial; antiviral; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200063377-A1.
XX
PD 26-OCT-2000.
XX
PF 19-APR-2000; 2000WO-US10454.
XX
PR 20-APR-1999; 99US-0294943.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Piddington CS, Bishop PD;
XX
DR WPI; 2000-665243/64.
XX
PT Novel zacrp3 polypeptides used to treat or prevent bacterial or viral
PT infections, for wound healing, improving blood flow, and to analyze
PT energy efficiency in mammals -
XX
PS Claim 10; Page 115; 123pp; English.
XX
CC The invention relates to the human zacrp3 protein (AAB29580) and to
CC nucleic acids which encode it (AAC64058, AAC64063). Zacrp3 is a homogue
CC of adipocyte complement related protein (ACRP30) and contains a
CC collagen-like domain comprising Gly-Xaa-Xaa or Gly-Xaa-Pro repeats, and a
CC C-terminal C1q domain comprising 10 beta-strands. The zacrp3 gene is
CC located on chromosome 5p12. The invention also relates to zacrp3
CC fragments, fusion proteins containing zacrp3 polypeptides,
CC zacrp3-specific antibodies, expression constructs and host cells
CC comprising zacrp3 nucleic acids, and methods of recombinant production of
CC zacrp3. Human zacrp3, and its agonists and antagonists may be used in the
CC study and modulation of cellular metabolism and energy balance in
CC mammals, and may therefore be used to treat disorders such as obesity and
CC anorexia, and conditions associated with these disorders. Due to its C1q
CC like domain, zacrp3 and zacrp3-containing fusion proteins may be useful
CC as antimicrobial agents, promoting lysis or phagocytosis of infectious
CC organisms such as bacteria or viruses. Zacrp3, its fragments, fusion
CC proteins, antibodies and activity modulators may also be used to inhibit
CC collagen-induced platelet aggregation, adhesion, or activation, and may
CC therefore have potential for promoting blood flow within the vasculature
CC of a mammal e.g., to treat injury to the vasculature or other collagenous
CC tissue. Human zacrp3 and its antibodies may additionally be used to study
CC dimerisation and oligomerisation. The present sequence represents a
CC degenerate DNA sequence encoding human zacrp3.
XX
SQ Sequence 738 BP; 130 A; 74 C; 145 G; 99 T; 290 other;

Query Match 31.8%; Score 544.2; DB 21; Length 738;
Best Local Similarity 60.7%; Pred. No. 7.9e-148;
Matches 448; Conservative 165; Mismatches 125; Indels 0; Gaps 0;

```
Qy      77 ATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTCCTCCCTTTTTGC 136
           |||:| |||:| ||::| ||:||:|||||::| :| || :| ||:||::| || ||:||:
Db       1 ATGYTNTGGMGNCARYTNATHTAYTGGCARYTNYTNGCNYTNTTYTTYYTNCCNTTYTGY 60

Qy     137 CTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGT 196
           :| ||:||:||:||:||:|||||::: || ||:|| || || :| || || ||:||::::
Db      61 YTNTGYCARGAYGARTAYATGGARWSNCCNCARACNGGNGGNYTNCCNCCNGAYTGYWSN 120

Qy     197 AAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCCTGGGCCACCGGGC 256
           ||:||:||:||:|| ||:||::: ||::| || ||:||:|| || || || || || || ||
Db     121 AARTGYTGYCAYGGNGAYTAYWSNTTYMGNGGNTAYCARGGNCCNCCNGGNCCNCCNGGN 180

Qy     257 CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAA 316
           || || || ||:|| || ||:||:|| ||:||:|| ||:||:|| || || || ||:||:
Db     181 CCNCCNGGNATHCCNGGNAAYCAYGGNAAYAAYGGNAAYAAYGGNGCNACNGGNCAYGAR 240

Qy     317 GGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAG 376
           || || ||:|| ||:||:|| ||:||:|| ||::| || || :| || ||::| || ||:
Db     241 GGNGCNAARGGNGARAARGGNGAYAARGGNGAYYTNGGNCCNMGNGGNGARMGNGGNCAR 300

Qy     377 CATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTC 436
           ||:|| || ||:|| ||:||:|| ||:|| || ||:|| || ||::| ||:||:|| ||:
Db     301 CAYGGNCCNAARGGNGARAARGGNTAYCCNGGNATHCCNCCNGARYTNCARATHGCNTTY 360

Qy     437 ATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTT 496
           ||||| :: :| || || ||:||::: ||:||:||::: || ||:||:||::: :: ||
Db     361 ATGGCNWSNYTNGCNACNCAYTTYWSNAAYCARAAYWSNGGNATHATHTTYWSNWSNGTN 420

Qy     497 GAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCA 556
           ||:|| ||:||:|| ||:||:||:||:|| ||||| || :| ||:|| || || || ::
Db     421 GARACNAAYATHGGNAAYTTYTTYGAYGTNATGACNGGNMGNTTYGGNGCNCCNGTNWSN 480

Qy     557 GGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTG 616
           || || ||:||:||:|| ||::: ||||||||:||:||:||:|| ||:||:|| ||:||
Db     481 GGNGTNTAYTTYTTYACNTTYWSNATGATGAARCAYGARGAYGTNGARGARGTNTAYGTN 540

Qy     617 TACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAA 676
           ||::| ||||:||:|| ||:|| || ||::: |||||::: ||:||:|||||:|| ||:
Db     541 TAYYTNATGCAYAAYGGNAAYACNGTNTTYWSNATGTAYWSNTAYGARATGAARGGNAAR 600

Qy     677 TCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTG 736
           :: ||:|| :: :: ||:||:|| || :| ||::| || ||:|| ||:||:|| |||:|
Db     601 WSNGAYACNWSNWSNAAYCAYGCNGTNYTNAARYTNGCNAARGGNGAYGARGTNTGGYTN 660

Qy     737 CGAATGGGCAATGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTC 796
           :| ||||| ||:|| || :| ||:|| ||:||:||::| ||::: || ||:|| || ||:
Db     661 MGNATGGGNAAYGGNGCNYTNCAYGGNGAYCAYCARMGNTTYWSNACNTTYGCNGGNTTY 720

Qy     797 CTGCTCTTTGAAACTAAG 814
           :| :| ||:||:|| ||:
Db     721 YTNYTNTTYGARACNAAR 738
```

```
RESULT 23
AAF94215/c
ID   AAF94215 standard; DNA; 552 BP.
XX
AC   AAF94215;
XX
DT   23-MAY-2001  (first entry)
XX
DE   Primer specific for DNA encoding secretory/membrane protein SEQ ID 649.
XX
KW   Human; secretory protein; membrane protein; vaccine; gene therapy;
KW   rheumatoid arthritis; diabetes; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   EP1067182-A2.
XX
PD   10-JAN-2001.
XX
PF   07-JUL-2000; 2000EP-0114090.
XX
PR   08-JUL-1999;   99JP-0194179.
PR   11-JAN-2000; 2000JP-0118775.
PR   02-MAY-2000; 2000JP-0183766.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
XX
DR   WPI; 2001-093989/11.
XX
PT   Nucleic acids encoding secretory proteins/membrane proteins, useful in
PT   gene therapy or as candidate target molecules in drug development -
XX
PS   Claim 5; SEQ ID 649; 609pp + CD ROM; English.
XX
CC   This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC   which encode human secretory or membrane proteins represented by
CC   AAB88317 - AAB88419. Included in the invention are primers
CC   AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
CC   cDNA sequences of the invention. The invention also includes methods for
CC   the production of antibodies directed against the proteins, and cDNA
CC   sequences, which can be used in vaccines. The polynucleotide sequences
CC   can be used in gene therapy. The polynucleotide sequences and the
CC   proteins they encode may be used in the prevention, treatment and
CC   diagnosis of diseases associated with inappropriate secretory
CC   protein/membrane protein expression. The nucleic acids and complementary
CC   sequences may also be used as DNA probes in diagnostic assays
CC   (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
CC   presence of similar nucleic acid sequences in samples. They may also be
CC   used to study the expression and function of secretory proteins/membrane
CC   polypeptides and their role in metabolism. The polypeptides may be used
CC   as antigens in the production of antibodies against them and in assays to
CC   identify modulators (agonists and antagonists) of expression and
CC   activity. The antibodies and antagonists may also be used as therapeutic
CC   agents to down regulate expression and activity. The antibodies may also
CC   be used as diagnostic agents for detecting the presence of the
CC   polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC   (ELISA). Examples of diseases which may be treated include rheumatoid
CC   arthritis and diabetes.
XX
SQ   Sequence 552 BP; 169 A; 105 C; 101 G; 170 T; 7 other;

  Query Match           29.1%;  Score 498.6;  DB 22;  Length 552;
  Best Local Similarity  96.9%;  Pred. No. 1.3e-134;
  Matches  526;  Conservative    0;  Mismatches   15;  Indels    2;  Gaps    2;

Qy   1156 TTAATTTAATACCAGTTTTCAGGAACCCCTGAAGTTTTAAGTTCATTATT-CTTTATAAC 1214
           || |  |    ||   || ||| |||||||||||||| |||| ||||||| ||||||| |
Db    542 TTTAANTTNANCCCAGTTNCAGNAACCCCTGAAGTTTNAAGTCCATTATTCCTTTATACC 483

Qy   1215 ATTTGAGAGAATCGGATGTAGTGATATGACAGGGCTGGGGCAAGAACAGGGGCACTAGCT 1274
          |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db    482 ATTTGAGAGAATCGGATGTAGTGATATG-CAGGGCTGGGGCAAGAACAGGGGCACTAGCT 424

Qy   1275 GCCTTATTAGCTAATTTAGTGCCCTCCGTGTTCAGCTTAGCCTTTGACCCTTTCCTTTTG 1334
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    423 GCCTTATTAGCTAATTTAGTGCCCTCCGTGTTCAGCTTAGCCTTTGACCCTTTCCTTTTG 364

Qy   1335 ATCCACAAAATACATTAAAACTCTGAATTCACATACAATGCTATTTTAAAGTCAATAGAT 1394
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    363 ATCCACAAAATACATTAAAACTCTGAATTCACATACAATGCTATTTTAAAGTCAATAGAT 304

Qy   1395 TTTAGCTATAAAGTGCTTGACCAGTAATGTGGTTGTAATTTTGTGTATGTTCCCCCACAT 1454
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    303 TTTAGCTATAAAGTGCTTGACCAGTAATGTGGTTGTAATTTTGTGTATGTTCCCCCACAT 244

Qy   1455 CGCCCCCAACTTCGGATGTGGGGTCAGGAGGTTGAGGTTCACTATTAACAAATGTCATAA 1514
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    243 CGCCCCCAACTTCGGATGTGGGGTCAGGAGGTTGAGGTTCACTATTAACAAATGTCATAA 184

Qy   1515 ATATCTCATAGAGGTACAGTGCCAATAGATATTCAAATGTTGCATGTTGACCAGAGGGAT 1574
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    183 ATATCTCATAGAGGTACAGTGCCAATAGATATTCAAATGTTGCATGTTGACCAGAGGGAT 124

Qy   1575 TTTATATCTGAAGAACATACACTATTAATAAATACCTTAGAGAAAGATTTTGACCTGGCT 1634
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    123 TTTATATCTGAAGAACATACACTATTAATAAATACCTTAGAGAAAGATTTTGACCTGGCT 64

Qy   1635 TTAGATAAAACTGTGGCAAGAAAAATGTAATGAGCAATATATGGAAATAAACACACCTTT 1694
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     63 TTAGATAAAACTGTGGCAAGAAAAATGTAATGAGCAATATATGGAAATAAACACACCTTT 4

Qy   1695 GTT 1697
          |||
Db       3 GTT 1

RESULT 24
AAC02874
ID   AAC02874 standard; cDNA; 471 BP.
XX
AC   AAC02874;
XX
DT   06-OCT-2000  (first entry)
XX
DE   Human secreted protein 5' EST, SEQ ID NO: 2872.
XX
KW   Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW   gene therapy; chromosome mapping; ss.
XX
OS   Homo sapiens.
XX
PN   EP1033401-A2.
XX
PD   06-SEP-2000.
XX
PF   21-FEB-2000; 2000EP-0200610.
XX
PR   26-FEB-1999;   99US-0122487.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR   WPI; 2000-500381/45.
DR   P-PSDB; AAG02868.
XX
PT   New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT   obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT   diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS   Claim 1; SEQ ID 2872; 71pp + CD-ROM; English.
XX
```

```
CC   The present sequence is one of a large number of 5' ESTs derived from
CC   mRNAs encoding secreted proteins. An ORF has been identified within the
CC   sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
CC   derived from 30 different tissues. EST sequences usually correspond
CC   mainly to the 3' untranslated region (UTR) of the mRNA because they are
CC   often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
CC   well suited for isolating cDNA sequences derived from the 5' ends of
CC   mRNAs and even in those cases where longer cDNA sequences have been
CC   obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
CC   mRNAs with intact 5' ends and can therefore be used to obtain full length
CC   cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
CC   gene therapy and chromosome mapping procedures. They are used to obtain
CC   upstream regulatory sequences and to design expression and secretion
CC   vectors.
XX
SQ   Sequence 471 BP; 107 A; 130 C; 134 G; 99 T; 1 other;

  Query Match             26.4%;  Score 452;  DB 21;  Length 471;
  Best Local Similarity   99.6%;  Pred. No. 4.4e-121;
  Matches  452;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GGCATCTGCCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12 GGCATCTGCCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGA 71

Qy      61 GGCTCTGTTGAGAATCATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72 GGCTCTGTTGAGAATCATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTT 131

Qy     121 TTTCCTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     132 TTTCCTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACT 191

Qy     181 ACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     192 ACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCC 251

Qy     241 CCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     252 CCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGG 311

Qy     301 AGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     312 AGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCG 371

Qy     361 AGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     372 AGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGA 431

Qy     421 ACTTCAGATTGCATTCATGGCTTCTCTGGCAACC 454
          |||||||||||||||||||||||||:| ||
Db     432 ACTTCAGATTGCATTCATGGCTTCTCTGGMACCC 465


RESULT 25
AAX39551
ID   AAX39551 standard; DNA; 472 BP.
XX
AC   AAX39551;
XX
DT   21-JUN-1999  (first entry)
XX
DE   Human secreted protein 5' EST SEQ ID No 149.
XX
KW   Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW   forensic; gene therapy; chromosome mapping; signal peptide;
KW   upstream regulatory sequence; cytokine activity; cell proliferation;
KW   differentiation; haematopoiesis regulation; tissue growth regulation;
KW   reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW   thrombolytic; anti-inflammatory; tumour inhibition; ds.
XX
OS   Homo sapiens.
XX
PN   WO9906551-A2.
XX
PD   11-FEB-1999.
XX
PF   31-JUL-1998;   98WO-IB01235.
XX
PR   01-AUG-1997;   97US-0905133.
XX
PA   (GEST ) GENSET.
XX
PI   Duclert A,  Dumas Milne Edwards J,  Lacroix B;
XX
DR   WPI; 1999-153781/13.
DR   P-PSDB; AAY11485.
XX
PT   New nucleic acids encoding human secreted - proteins obtained from
PT   cDNA libraries prepared from substantia nigra, cerebellum, surrenals
PT   and fetal brain tissue
XX
PS   Claim 1; Page 263; 434pp; English.
XX
CC   AAX39440 to AAX39597 represent 5' expressed sequence tags (ESTs) for
CC   human secreted proteins, and encode the proteins given in AAY11374 to
CC   AAY11531, respectively. The proteins given represent the signal peptide
CC   and an N-terminal fragment of a secreted protein. The nucleic acid
CC   sequences can be used for producing secreted human gene products. They
CC   can also be used to develop products for diagnosis and therapy. The
CC   proteins obtained may have cytokine activity, cell
CC   proliferation/differentiation activity, haematopoiesis regulating
CC   activity, tissue growth regulating activity, reproductive hormone
CC   regulating activity, chemotactic/ chemokinetic activity, haemostatic and
CC   thrombolytic activity, receptor/ ligand activity, anti-inflammatory
CC   activity, tumour inhibition activity or other activities. The products
CC   can be used in forensic, gene therapy and chromosome mapping procedures.
CC   The sequences can also be used for obtaining corresponding promoter
CC   sequences. The nucleic acids encoding the signal peptide can be used for
CC   directing extracellular secretion of a polypeptide or the insertion of a
CC   polypeptide into a membrane, or importing a polypeptide into a cell.
XX
SQ   Sequence 472 BP; 108 A; 130 C; 134 G; 99 T; 1 other;

  Query Match             26.4%;  Score 452;  DB 20;  Length 472;
  Best Local Similarity   99.6%;  Pred. No. 4.4e-121;
  Matches  452;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GGCATCTGCCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13 GGCATCTGCCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGA 72

Qy      61 GGCTCTGTTGAGAATCATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73 GGCTCTGTTGAGAATCATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTT 132

Qy     121 TTTCCTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     133 TTTCCTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACT 192

Qy     181 ACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     193 ACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCC 252

Qy     241 CCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     253 CCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGG 312

Qy     301 AGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     313 AGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCG 372

Qy     361 AGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     373 AGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGA 432
```

```
Qy    421 ACTTCAGATTGCATTCATGGCTTCTCTGGCAACC 454
          ||||||||||||||||||||||||||||||:| ||
Db    433 ACTTCAGATTGCATTCATGGCTTCTCTGGMACCC 466
```

RESULT 26
ABV56781
ID  ABV56781 standard; cDNA; 472 BP.
XX
AC  ABV56781;
XX
DT  17-SEP-2002  (first entry)
XX
DE  Human prostate expression marker cDNA 56772.
XX
KW  Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW  pharmacogenomic marker; gene; ss.
XX
OS  Homo sapiens.
XX
PN  WO200160860-A2.
XX
PD  23-AUG-2001.
XX
PF  20-FEB-2001; 2001WO-US05171.
XX
PR  17-FEB-2000; 2000US-183319P.
PR  16-MAR-2000; 2000US-189862P.
PR  25-MAY-2000; 2000US-207454P.
PR  09-JUN-2000; 2000US-211314P.
PR  18-JUL-2000; 2000US-219007P.
PR  13-DEC-2000; 2000US-255281P.
XX
PA  (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI  Schlegel R,  Endege WO,  Monahan JE;
XX
DR  WPI; 2001-662795/76.
XX
PT  Novel isolated nucleic acid molecule associated with cancerous state of
PT  prostate cells and correlating with presence of prostate cancer, useful
PT  for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS  Claim 1; Page 10943; 11750pp; English.
XX
CC  The invention relates to an isolated nucleic acid molecule (I) comprising
CC  a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC  specification or its complement. (I) is useful for:
CC  (a) assessing whether a patient is afflicted with prostate cancer;
CC  (b) monitoring the progression of prostate cancer in a patient;
CC  (c) assessing the efficacy of a test compound to inhibit prostate
CC  cancer in a patient;
CC  (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC  in a patient;
CC  (e) selecting a composition for inhibiting prostate cancer in a patient;
CC  (f) assessing the prostate cell carcinogenic potential of a compound;
CC  (g) determining whether prostate cancer has metastasized in a patient;
CC  (h) assessing the aggressiveness or indolence of prostate cancer in a
CC  patient;
CC  (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
XX
SQ  Sequence 472 BP; 141 A; 105 C; 92 G; 134 T; 0 other;

Query Match  20.2%;  Score 345.6;  DB 23;  Length 472;
Best Local Similarity  87.7%;  Pred. No. 4.4e-90;
Matches 400;  Conservative  0;  Mismatches  54;  Indels  2;  Gaps  2;

```
Qy    587 AAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATGG-CAACACAGT-CT 644
          || |||||||||||| |||||||||| ||||| |||||||||||||| ||||||||| ||
Db     17 AACCATGAGGATGTGGAGGAAGTGTTTGTGTTCCTTATGCACAATGGCCAACACAGTCCT 76

Qy    645 TCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCAATCATGCTGTGC 704
          ||||||||| ||| ||| ||| |||||||||||||| || | |||| || || | ||||||
Db     77 TCAGCATGTCCAGTTATAAAAGGAAGGGCAAATCAAATCCTTCCACCATTCTTCCTGTGC 136

Qy    705 TGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTCCATGGGG 764
          | || ||| |||||||||||| ||||| | |||| |||||||||||||| || || ||||||
Db    137 TAAACCTACCCAAAGGGGATAAGGTTGGCCTGCAAATGGGCAATGGCTCTTTCTATGGGG 196

Qy    765 ACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTAAGTAAATATATG 824
          |||||||||||||||||| |||||||||| |||||| |||||| |||| ||||||| ||
Db    197 ACCACCAACGCTTCTCCACTTTTGCAGGATCCCTGCTTTTTGAACCTAATTAAATATTTG 256

Qy    825 ACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCTGATTTGTTACGATCTGAGG 884
          |||| |||  ||||| |||||| || ||||||| |||| |||||||||| | ||||||||
Db    257 ACTAAAATCCCTCCATTTTGGGAAAAACTTGTACCTGACCTGATTTGTTCCAATCTGAGG 316

Qy    885 AACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATTATTGGTTGCAATGTTGT 944
          |||||||||| |||||||||| ||||||||  |||||||||| ||||||||||||||||
Db    317 AACATTAAAGTGGAGGGTTTTACTTTGCTGTATAAAAAAAATTATGGGTTGCAATGTTGT 376

Qy    945 TCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGAAGAATCAACCACA 1004
          |||| ||||||| |||||||||||||||||||||||||||||||| || | ||| |||||
Db    377 TCACCCTACAGGCACACCAATAATGTTGGACAATTCAGGGGCTCAAAAAACTCACCCACA 436

Qy   1005 AAATAGTCTTCTCAGATGACCTTGACTAATATACTC 1040
          ||||||| |||||| ||||||||||||||||||||
Db    437 AAATAGTTTTCTCAAATGACCTTGACTAATATACTC 472
```

RESULT 27
AAF93419
ID  AAF93419 standard; cDNA; 546 BP.
XX
AC  AAF93419;
XX
DT  21-MAY-2001  (first entry)
XX
DE  cDNA encoding SRT protein isolated from prostate tissue SEQ ID 240.
XX
KW  Human; SRT; gene therapy; gene mapping; tissue typing; ss.
XX
OS  Homo sapiens.
XX
PN  WO200107611-A2.
XX
PD  01-FEB-2001.
XX
PF  21-JUL-2000; 2000WO-US20006.
XX
PR  26-JUL-1999;  99US-0145701.
XX
PA  (GETH ) GENENTECH INC.
XX
PI  Baker KP,  Goddard A,  Wood WI;
XX
DR  WPI; 2001-112729/12.
XX
PT  New isolated nucleic acid molecule encoding a SRT polypeptide is useful
PT  for production of recombinant SRT polypeptides, gene mapping,
PT  diagnosing genetic disorders and for gene therapy -
XX
PS  Claim 2; Fig 240; 663pp; English.
XX
CC  Sequences AAF93180 - AAF93743 represent polynucleotide sequences encoding
CC  human SRT proteins. The cDNA sequences are isolated from various
CC  different human tissue cDNA libraries. The invention relates to a method
CC  for detecting cDNA encoding an SRT protein, a vector containing cDNA
CC  encoding SRT, a host cell transformed with the vector, an isolated SRT
CC  polypeptide, and an antibody which binds to SRT. The polynucleotide
CC  sequence can be used in gene therapy and is useful in the recombinant
CC  production of SRT polypeptides, as a hybridisation probe to screen
CC  libraries to isolate cDNAs with sequence identity to SRT polypeptides, to
CC  map the gene encoding the SRT polypeptides and analysing genetic
CC  disorders, tissue typing and disease tissue detection. The SRT
CC  polynucleotide sequences can be used in polymerase chain reaction,

```
CC   screening for new therapeutic molecules and generation of antisense RNA
CC   and DNA.
XX
SQ   Sequence 546 BP; 149 A; 129 C; 155 G; 108 T; 5 other;

  Query Match            12.1%;  Score 208;  DB 22;  Length 546;
  Best Local Similarity   99.5%;  Pred. No. 5.9e-50;
  Matches  208;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     159 AGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTACA 218
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     338 AGTNTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTACA 397

Qy     219 GCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACC 278
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     398 GCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACC 457

Qy     279 ATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCG 338
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     458 ATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCG 517

Qy     339 ACAAAGGTGACCTGGGGCCTCGAGGGGAG 367
           |||||||||||||||||||||||||||||
Db     518 ACAAAGGTGACCTGGGGCCTCGAGGGGAG 546


RESULT 28
ABA60188
ID   ABA60188 standard; DNA; 548 BP.
XX
AC   ABA60188;
XX
DT   01-FEB-2002  (first entry)
XX
DE   Human foetal liver single exon nucleic acid probe #8493.
XX
KW   Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157277-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00669.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-483447/52.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human fetal liver -
XX
PS   Claim 1; SEQ ID NO 8493; 639pp + sequence listing; English.
XX
CC   The invention relates to a single exon nucleic acid probe for
CC   measuring human gene expression in a sample derived from human foetal
CC   liver. The single exon nucleic acid probes may be used for predicting,
CC   measuring and displaying gene expression in samples derived from human
CC   fetal liver. The present sequence is a single exon nucleic acid
CC   probe of the invention.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 548 BP; 182 A; 81 C; 101 G; 184 T; 0 other;

  Query Match             8.0%;  Score 136.2;  DB 22;  Length 548;
  Best Local Similarity   97.9%;  Pred. No. 4.9e-29;
  Matches  138;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     422 CTTCAGATTGCATTCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATT 481
           | | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     326 CCTTAGATTGCATTCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATT 385

Qy     482 ATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTT 541
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     386 ATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTT 445

Qy     542 GGGGCCCCAGTATCAGGTGTG 562
           |||||||||||||||||| |
Db     446 GGGGCCCCAGTATCAGGTGAG 466


RESULT 29
AAK08465
ID   AAK08465 standard; DNA; 548 BP.
XX
AC   AAK08465;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Human brain expressed single exon probe SEQ ID NO: 8456.
XX
KW   Human; brain expressed exon; gene expression analysis; probe;
KW   microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW   epilepsy; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157275-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00667.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-483446/52.
XX
PT   Single exon nucleic acid probes for analyzing gene expression in human
PT   brains -
XX
PS   Example 4; SEQ ID NO: 8456; 650pp + Sequence Listing; English.
XX
CC   The present invention provides a number of single exon nucleic acid
CC   probes which are derived from genomic sequences expressed in the human
CC   brain. They can be used to measure gene expression in brain cell samples,
CC   which may enable the diagnosis and improved treatment of nervous system
CC   diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC   epilepsy and cancers. The present sequence is one of the probes of the
CC   invention.
XX
SQ   Sequence 548 BP; 182 A; 81 C; 101 G; 184 T; 0 other;

  Query Match             8.0%;  Score 136.2;  DB 22;  Length 548;
```

```
  Best Local Similarity   97.9%;  Pred. No. 4.9e-29;
  Matches  138;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     422 CTTCAGATTGCATTCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATT 481
           | | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     326 CCTTAGATTGCATTCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATT 385

Qy     482 ATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTT 541
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     386 ATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTT 445

Qy     542 GGGGCCCCAGTATCAGGTGTG 562
           |||||||||||||||||||| |
Db     446 GGGGCCCCAGTATCAGGTGAG 466


RESULT 30
AAK34347
ID   AAK34347 standard; DNA; 548 BP.
XX
AC   AAK34347;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human bone marrow expressed single exon probe SEQ ID NO: 8904.
XX
KW   Human; bone marrow expressed exon; gene expression analysis; probe;
KW   microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157276-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00668.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488900/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human bone marrow -
XX
PS   Example 4; SEQ ID NO: 8904; 658pp + Sequence Listing; English.
XX
CC   The present invention provides a number of single exon nucleic acid
CC   probes which are derived from genomic sequences expressed in the human
CC   bone marrow. They can be used to measure gene expression in bone marrow
CC   samples, which may enable the improved diagnosis and treatment of cancers
CC   such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC   the probes of the invention.
XX
SQ   Sequence 548 BP; 182 A; 81 C; 101 G; 184 T; 0 other;

  Query Match             8.0%;  Score 136.2;  DB 22;  Length 548;
  Best Local Similarity   97.9%;  Pred. No. 4.9e-29;
  Matches  138;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     422 CTTCAGATTGCATTCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATT 481
           | | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     326 CCTTAGATTGCATTCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATT 385

Qy     482 ATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTT 541
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     386 ATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTT 445

Qy     542 GGGGCCCCAGTATCAGGTGTG 562
           |||||||||||||||||||| |
Db     446 GGGGCCCCAGTATCAGGTGAG 466


Search completed: March 13, 2003, 15:58:42
Job time : 441 secs
```

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 13, 2003, 16:22:07 ; Search time 263 Seconds
(without alignments)
2106.432 Million cell updates/sec

Title: US-10-036-041-2
Perfect score: 1367
Sequence: 1 MLWRQLIYWQLLALFFLPFC.....LHGDHQRFSTFAGFLLFETK 246

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10036041/runat_06032003_154638_21993/app_query.fasta_1.391
-DB=N_Geneseq_101002 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=30
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10036041_@CGN_1_1_263_@runat_06032003_154638_21993 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| | 1 | 1367 | 100.0 | 741 | 24 | ABK35591 | Gene encoding nove |
| | 2 | 1367 | 100.0 | 1696 | 21 | AAC64058 | Human zacrp3 cDNA, |
| | 3 | 1367 | 100.0 | 1709 | 22 | AAF93874 | Human cDNA encodin |
| | 4 | 1367 | 100.0 | 1712 | 21 | AAA96336 | cDNA encoding a no |
| | 5 | 1367 | 100.0 | 1760 | 21 | AAA95787 | Human immune syste |
| | 6 | 1320.5 | 96.6 | 960 | 24 | ABK35590 | Gene encoding nove |
| | 7 | 1311 | 95.9 | 1035 | 22 | AAC99776 | Skin cell cDNA, SE |
| | 8 | 1311 | 95.9 | 1035 | 24 | ABL34928 | Rat cDNA isolated |
| | 9 | 1311 | 95.9 | 1117 | 21 | AAC64064 | Mouse zacrp2 DNA, |
| | 10 | 1311 | 95.9 | 1123 | 21 | AAZ61633 | cDNA encoding rat |
| | 11 | 1311 | 95.9 | 1123 | 21 | AAZ61730 | cDNA encoding rat |
| | 12 | 1311 | 95.9 | 1123 | 22 | AAC99566 | Skin cell cDNA, SE |
| | 13 | 1311 | 95.9 | 1123 | 22 | AAC99663 | Skin cell cDNA, SE |
| | 14 | 1311 | 95.9 | 1123 | 24 | ABL34718 | Rat cDNA isolated |
| | 15 | 1311 | 95.9 | 1123 | 24 | ABL34815 | Rat cDNA isolated |
| | 16 | 1291.5 | 94.5 | 1927 | 22 | AAD12584 | Human protein havi |
| | 17 | 1259 | 92.1 | 810 | 22 | AAF94076 | Primer specific fo |
| | 18 | 1211 | 88.6 | 1792 | 22 | AAI59230 | Human polynucleoti |
| | 19 | 1208 | 88.4 | 1620 | 22 | AAI99523 | Human polynucleoti |
| | 20 | 1171 | 85.7 | 738 | 21 | AAC64063 | Human zacrp3 degen |
| c | 21 | 858.5 | 62.8 | 1799 | 22 | AAI61016 | Human polynucleoti |
| | 22 | 849 | 62.1 | 1608 | 24 | ABK35221 | Human cDNA encodin |
| | 23 | 721 | 52.7 | 471 | 21 | AAC02874 | Human secreted pro |
| | 24 | 721 | 52.7 | 472 | 20 | AAX39551 | Human secreted pro |
| | 25 | 513.5 | 37.6 | 546 | 22 | AAF93419 | cDNA encoding SRT |
| | 26 | 325 | 23.8 | 804 | 24 | ABK35598 | Gene encoding nove |
| | 27 | 316 | 23.1 | 1107 | 21 | AAZ61744 | cDNA encoding rat |
| | 28 | 316 | 23.1 | 1107 | 22 | AAC99677 | Skin cell cDNA, SE |
| | 29 | 316 | 23.1 | 1107 | 24 | ABL34829 | Rat cDNA isolated |
| | 30 | 315 | 23.0 | 870 | 22 | AAD16350 | Human SBhACRP30a g |
| | 31 | 315 | 23.0 | 870 | 24 | ABQ86182 | Novel human gene. |
| | 32 | 315 | 23.0 | 912 | 22 | AAD16351 | Human SBhACRP30a g |
| | 33 | 315 | 23.0 | 912 | 22 | AAC89867 | Human zacrp7 cDNA. |
| | 34 | 315 | 23.0 | 1242 | 24 | AAL44067 | Human genset metab |
| | 35 | 315 | 23.0 | 1297 | 24 | ABK94966 | Human novel polynu |
| | 36 | 313 | 22.9 | 855 | 21 | AAC67788 | Murine ACRP30R1M c |
| | 37 | 309 | 22.6 | 1282 | 22 | AAC89875 | Mouse zacrp7 cDNA. |
| | 38 | 306 | 22.4 | 1052 | 21 | AAZ61811 | cDNA encoding rat |
| | 39 | 306 | 22.4 | 1052 | 22 | AAC99744 | Skin cell cDNA, SE |
| | 40 | 306 | 22.4 | 1052 | 24 | ABL34896 | Rat cDNA isolated |
| | 41 | 306 | 22.4 | 1161 | 21 | AAC65132 | Human adipocyte co |
| | 42 | 306 | 22.4 | 1171 | 22 | AAS31128 | Human diagnostic a |
| | 43 | 306 | 22.4 | 1171 | 24 | ABQ54564 | Human ovarian anti |
| | 44 | 304 | 22.2 | 932 | 21 | AAZ45606 | cDNA encoding poly |
| | 45 | 299 | 21.9 | 1276 | 18 | AAT51048 | Murine adipocyte c |

ALIGNMENTS

RESULT 1
ABK35591
ID ABK35591 standard; DNA; 741 BP.
XX
AC ABK35591;
XX
DT 08-MAY-2002 (first entry)
XX
DE Gene encoding novel human secreted or membrane-associated protein #10.
XX
KW Human; secreted protein; membrane-associated protein; hypertension;
KW inflammatory disorder; neurological disorder; haematopoietic disorder;
KW skeletal developmental disorder; growth abnormality; autoimmune disorder;
KW neurodegenerative disorder; nervous system disorder; bacterial infection;
KW peripheral myelinopathy; viral infection; cancer; obesity; diabetes;
KW hypotension; sexual development disorder; blood disorder; gene; ds.
XX
OS Homo sapiens.

```
XX
PN   WO200204600-A2.
XX
PD   17-JAN-2002.
XX
PF   12-JUL-2001; 2001WO-US21985.
XX
PR   12-JUL-2000; 2000US-218033P.
PR   21-AUG-2000; 2000US-226517P.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
PA   (GLAX ) GLAXO GROUP LTD.
XX
PI   Agarwal P,  Cogswell JP,  Lai Y,  Martensen SA,  Rizvi SK,  Strum JC;
PI   Smith RF,  Xiang Z,  Xie Q;
XX
DR   WPI; 2002-188468/24.
DR   P-PSDB; AAU84371.
XX
PT   Novel secreted and membrane-associated polypeptides and polynucleotides
PT   encoding the polypeptides, for preventing, treating and ameliorating
PT   cancers, mental or sexual developmental disorders, and malignant tumours
PT   -
XX
PS   Claim 2; Page 106; 151pp; English.
XX
CC   The present invention relates to the isolation of novel human secreted
CC   or membrane-associated proteins and the genes encoding them. The
CC   sequences of the invention are useful for treating, preventing and
CC   ameliorating various diseases such as inflammatory disorders (e.g.
CC   asthma), neurological disorders (e.g. dementia), haematopoietic
CC   disorders, skeletal developmental disorders, growth abnormalities,
CC   neurodegenerative disorders (e.g. Huntington's disease), nervous system
CC   disorders, autoimmune disorders (e.g. rheumatoid arthritis),
CC   peripheral myelinopathies, viral and bacterial infections,
CC   alpha-mannosidosis, diabetes, cancers, malignant tumours, hyper- and
CC   hypotension, obesity, bulimia, anorexia, manic depression, delirium,
CC   mental retardation, Tourette's syndrome, schizophrenia, growth, mental
CC   or sexual development disorders, and dysfunctions of the blood cascade
CC   system including those leading to stroke. ABK35582-ABK35609 represent
CC   the genes encoding the novel human secreted or membrane-associated
CC   proteins of the invention.
XX
SQ   Sequence 741 BP; 191 A; 178 C; 200 G; 172 T; 0 other;

Alignment Scores:
Pred. No.:                7.45e-100      Length:          741
Score:                    1367.00        Matches:         246
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       24             Gaps:            0

US-10-036-041-2 (1-246) x ABK35591 (1-741)

Qy       1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTCCTCCCTTTTGC 60

Qy      21 LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGT 120

Qy      41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGC 180

Qy      61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAA 240

Qy      81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAG 300

Qy     101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTC 360

Qy     121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 ATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTT 420

Qy     141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCA 480

Qy     161 GlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluValTyrVal 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTG 540

Qy     181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 TACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAA 600

Qy     201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTrpLeu 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTG 660

Qy     221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CGAATGGGCAATGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTC 720

Qy     241 LeuLeuPheGluThrLys 246
           ||||||||||||||||||
Db     721 CTGCTCTTTGAAACTAAG 738

RESULT 2
AAC64058
ID   AAC64058 standard; cDNA; 1696 BP.
XX
AC   AAC64058;
XX
DT   19-FEB-2001  (first entry)
XX
DE   Human zacrp3 cDNA, SEQ ID NO:1.
XX
KW   Human zacrp3; adipocyte complement related protein homologue;
KW   ACRP30; C1q domain; collagen-like domain; energy balance modulation;
KW   cellular metabolism; metabolic disorder; obesity; anorexia;
KW   antimicrobial agent; infection; platelet aggregation inhibition;
KW   adhesion; activation; vascular injury; antibacterial; antiviral; ss.
XX
OS   Homo sapiens.
XX
PN   WO200063377-A1.
XX
PD   26-OCT-2000.
XX
PF   19-APR-2000; 2000WO-US10454.
XX
PR   20-APR-1999;   99US-0294943.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Piddington CS,  Bishop PD;
XX
DR   WPI; 2000-665243/64.
DR   P-PSDB; AAB29580.
XX
PT   Novel zacrp3 polypeptides used to treat or prevent bacterial or viral
PT   infections, for wound healing, improving blood flow, and to analyze
PT   energy efficiency in mammals -
XX
PS   Claim 31; Page 107-109; 123pp; English.
```

```
XX
CC   The invention relates to the human zacrp3 protein (AAB29580) and to
CC   nucleic acids which encode it (AAC64058, AAC64063). Zacrp3 is a homogue
CC   of adipocyte complement related protein (ACRP30) and contains a
CC   collagen-like domain comprising Gly-Xaa-Xaa or Gly-Xaa-Pro repeats, and a
CC   C-terminal C1q domain comprising 10 beta-strands. The zacrp3 gene is
CC   located on chromosome 5p12. The invention also relates to zacrp3
CC   fragments, fusion proteins containing zacrp3 polypeptides,
CC   zacrp3-specific antibodies, expression constructs and host cells
CC   comprising zacrp3 nucleic acids, and methods of recombinant production of
CC   zacrp3. Human zacrp3, and its agonists and antagonists may be used in the
CC   study and modulation of cellular metabolism and energy balance in
CC   mammals, and may therefore be used to treat disorders such as obesity and
CC   anorexia, and conditions associated with these disorders. Due to its C1q
CC   like domain, zacrp3 and zacrp3-containing fusion proteins may be useful
CC   as antimicrobial agents, promoting lysis or phagocytosis of infectious
CC   organisms such as bacteria or viruses. Zacrp3, its fragments, fusion
CC   proteins, antibodies and activity modulators may also be used to inhibit
CC   collagen-induced platelet aggregation, adhesion, or activation, and may
CC   therefore have potential for promoting blood flow within the vasculature
CC   of a mammal e.g., to treat injury to the vasculature or other collagenous
CC   tissue. Human zacrp3 and its antibodies may additionally be used to study
CC   dimerisation and oligomerisation. The present sequence represents cDNA
CC   encoding human zacrp3.
XX
SQ   Sequence 1696 BP; 482 A; 355 C; 386 G; 473 T; 0 other;

Alignment Scores:
Pred. No.:                1.94e-99        Length:          1696
Score:                    1367.00         Matches:         246
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       21              Gaps:            0

US-10-036-041-2 (1-246) x AAC64058 (1-1696)

Qy       1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      69 ATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTCCTCCCTTTTTGC 128

Qy      21 LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     129 CTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGT 188

Qy      41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     189 AAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGC 248

Qy      61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     249 CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAA 308

Qy      81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     309 GGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAG 368

Qy     101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     369 CATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTC 428

Qy     121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     429 ATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTT 488

Qy     141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     489 GAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCA 548

Qy     161 GlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluValTyrVal 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     549 GGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTG 608

Qy     181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     609 TACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAA 668

Qy     201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTrpLeu 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     669 TCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTG 728

Qy     221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     729 CGAATGGGCAATGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTC 788

Qy     241 LeuLeuPheGluThrLys 246
           ||||||||||||||||||
Db     789 CTGCTCTTTGAAACTAAG 806

RESULT 3
AAF93874
ID   AAF93874 standard; cDNA; 1709 BP.
XX
AC   AAF93874;
XX
DT   23-MAY-2001  (first entry)
XX
DE   Human cDNA encoding a membrane or secretory protein clone PSEC0232.
XX
KW   Human; secretory protein; membrane protein; vaccine; gene therapy;
KW   rheumatoid arthritis; diabetes; ss.
XX
OS   Homo sapiens.
XX
PN   EP1067182-A2.
XX
PD   10-JAN-2001.
XX
PF   07-JUL-2000; 2000EP-0114090.
XX
PR   08-JUL-1999;   99JP-0194179.
PR   11-JAN-2000; 2000JP-0118775.
PR   02-MAY-2000; 2000JP-0183766.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Kawai Y,  Sugiyama T,  Hayashi K;
XX
DR   WPI; 2001-093989/11.
DR   P-PSDB; AAB88447.
XX
PT   Nucleic acids encoding secretory proteins/membrane proteins, useful in
PT   gene therapy or as candidate target molecules in drug development -
XX
PS   Claim 1; SEQ ID 261; 609pp + CD ROM; English.
XX
CC   This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC   which encode human secretory or membrane proteins represented by
CC   AAB88317 - AAB88419. Included in the invention are primers
CC   AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
CC   cDNA sequences of the invention. The invention also includes methods for
CC   the production of antibodies directed against the proteins, and cDNA
CC   sequences, which can be used in vaccines. The polynucleotide sequences
CC   can be used in gene therapy. The polynucleotide sequences and the
CC   proteins they encode may be used in the prevention, treatment and
CC   diagnosis of diseases associated with inappropriate secretory
CC   protein/membrane protein expression. The nucleic acids and complementary
CC   sequences may also be used as DNA probes in diagnostic assays
CC   (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
CC   presence of similar nucleic acid sequences in samples. They may also be
CC   used to study the expression and function of secretory proteins/membrane
CC   polypeptides and their role in metabolism. The polypeptides may be used
CC   as antigens in the production of antibodies against them and in assays to
CC   identify modulators (agonists and antagonists) of expression and
CC   activity. The antibodies and antagonists may also be used as therapeutic
CC   agents to down regulate expression and activity. The antibodies may also
```

```
CC   be used as diagnostic agents for detecting the presence of the
CC   polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC   (ELISA). Examples of diseases which may be treated include rheumatoid
CC   arthritis and diabetes.
XX
SQ   Sequence 1709 BP; 480 A; 363 C; 390 G; 476 T; 0 other;

Alignment Scores:
Pred. No.:              1.96e-99      Length:         1709
Score:                  1367.00       Matches:        246
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            100.00%       Indels:         0
DB:                     22            Gaps:           0

US-10-036-041-2 (1-246) x AAF93874 (1-1709)

Qy       1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      89 ATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTCCTCCCTTTTTGC 148

Qy      21 LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     149 CTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGT 208

Qy      41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     209 AAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGC 268

Qy      61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     269 CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAA 328

Qy      81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     329 GGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAG 388

Qy     101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     389 CATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTC 448

Qy     121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     449 ATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTT 508

Qy     141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     509 GAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCA 568

Qy     161 GlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluValTyrVal 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     569 GGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTG 628

Qy     181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     629 TACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAA 688

Qy     201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTrpLeu 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     689 TCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTG 748

Qy     221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     749 CGAATGGGCAATGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTC 808

Qy     241 LeuLeuPheGluThrLys 246
           ||||||||||||||||||
Db     809 CTGCTCTTTGAAACTAAG 826

RESULT 4
AAA96336
ID   AAA96336 standard; cDNA; 1712 BP.
XX
AC   AAA96336;
XX
DT   08-FEB-2001  (first entry)
XX
DE   cDNA encoding a novel polypeptide designated PRO1484.
XX
KW   Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122;
KW   PRO1889; PRO1890; PRO1887; PRO1785; PRO4353; PRO4357; PRO4405; PRO4356;
KW   PRO4352; PRO4380; PRO4354; PRO4408; PRO5737; PRO4425; PRO5990; PRO6030;
KW   PRO4424; PRO4422; PRO4430; PRO4499; tumour; obesity; diabetes;
KW   insulinemia; kidney disorder; Bergers disease; nephropathy;
KW   Schonlein-Henoch purpura; celiac disease; dermatitis herpetiformis;
KW   Crohns disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             77..817
FT                   /*tag=  a
FT   sig_peptide     77..142
FT                   /*tag=  b
XX
PN   WO200056889-A2.
XX
PD   28-SEP-2000.
XX
PF   01-MAR-2000; 2000WO-US05601.
XX
PR   23-MAR-1999;   99US-0125774.
PR   23-MAR-1999;   99US-0125778.
PR   24-MAR-1999;   99US-0125826.
PR   31-MAR-1999;   99US-0127035.
PR   05-APR-1999;   99US-0127706.
PR   21-APR-1999;   99US-0130359.
PR   27-APR-1999;   99US-0131270.
PR   27-APR-1999;   99US-0131272.
PR   27-APR-1999;   99US-0131291.
PR   04-MAY-1999;   99US-0132371.
PR   04-MAY-1999;   99US-0132379.
PR   04-MAY-1999;   99US-0132383.
PR   25-MAY-1999;   99US-0135750.
PR   08-JUN-1999;   99US-0138166.
PR   20-JUL-1999;   99US-0144791.
PR   03-AUG-1999;   99US-0146970.
PR   09-DEC-1999;   99US-0170262.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Desnoyers L,  Eaton DL,  Goddard A,  Godowski PJ,  Gurney AL,  Pan J;
PI   Stewart TA,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2000-628263/60.
DR   P-PSDB; AAB18909.
XX
PT   Novel secreted and transmembrane polypeptides useful for diagnosing
PT   tumour in a mammal, for identifying agonists and antagonists of the
PT   polypeptide and for therapeutic use
XX
PS   Claim 2; Fig 1; 222pp; English.
XX
CC   The present sequence encodes a secreted or transmembrane polypeptide.
CC   The specification describes polypeptides designated PRO1484, PRO4334,
CC   PRO1122, PRO1889, PRO1890, PRO1887, PRO1785, PRO4353, PRO4357, PRO4405,
CC   PRO4356, PRO4352, PRO4380, PRO4354, PRO4408, PRO5737, PRO4425, PRO5990,
CC   PRO6030, PRO4424, PRO4422, PRO4430 and PRO4499. PRO1889 polypeptide is
CC   useful for diagnosing tumour in a mammal. The polypeptides, their
CC   agonists and antagonists are useful treating a condition associated with
CC   expression or activity of the polypeptide. Conditions treated include
CC   obesity, diabetes or hyper-or hypo-insulinemia. The polypeptides are
CC   capable of inducing proliferation of mammalian kidney mesangial cells
CC   and are therefore useful for treating kidney disorders associated with
CC   decreased mesangial cell function such as Bergers disease or other
CC   nephropathies associated with Schonlein-Henoch purpura, celiac disease,
```

```
CC   dermatitis herpetiformis or Crohns disease. The nucleic acids may be used
CC   to generate transgenic animals for use in development and screening of
CC   therapeutically useful reagents and also for chromosome identification
CC   and tissue typing.
XX
SQ   Sequence 1712 BP; 491 A; 358 C; 388 G; 475 T; 0 other;

Alignment Scores:
Pred. No.:                1.96e-99        Length:          1712
Score:                    1367.00         Matches:         246
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       21              Gaps:            0

US-10-036-041-2 (1-246) x AAA96336 (1-1712)

Qy       1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      77 ATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTCCTCCCTTTTTGC 136

Qy      21 LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     137 CTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGT 196

Qy      41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     197 AAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGC 256

Qy      61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     257 CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAA 316

Qy      81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     317 GGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAG 376

Qy     101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     377 CATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTC 436

Qy     121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     437 ATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTT 496

Qy     141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     497 GAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCA 556

Qy     161 GlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluValTyrVal 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     557 GGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTG 616

Qy     181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     617 TACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAA 676

Qy     201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTrpLeu 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     677 TCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTG 736

Qy     221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     737 CGAATGGGCAATGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTC 796

Qy     241 LeuLeuPheGluThrLys 246
           ||||||||||||||||||
Db     797 CTGCTCTTTGAAACTAAG 814

RESULT 5
AAA95787
ID   AAA95787 standard; cDNA; 1760 BP.
XX
AC   AAA95787;
XX
DT   28-FEB-2001  (first entry)
XX
DE   Human immune system molecule cDNA from Incyte clone 1890540.
XX
KW   Anti-inflammatory; keratolytic; anti-HIV; anti-allergic; antianaemic;
KW   antiarteriosclerotic; antiasthmatic; antidiabetic; nephrotropic; cancer;
KW   antigout; dermatological; antithyroid; virucide; hepatotropic; antibody;
KW   immunosuppressive; cytostatic; fungicide; protozoacide; antibacterial;
KW   gene therapy; diagnostic; immunological disorder; viral infection; ss;
KW   bacterial infection; fungal infection; parasitic infection; immunogen.
XX
OS   Homo sapiens.
XX
PN   WO200060080-A2.
XX
PD   12-OCT-2000.
XX
PF   04-APR-2000; 2000WO-US09072.
XX
PR   05-APR-1999;   99US-0127852.
PR   05-MAY-1999;   99US-0132647.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Yue H,  Lal P,  Tang YT,  Baughn MR,  Azimzai Y,  Lu DAM;
XX
DR   WPI; 2000-665005/64.
DR   P-PSDB; AAB15548.
XX
PT   New human immune system molecules 1-15 and polynucleotides encoding
PT   them useful for diagnosing, treating or preventing e.g. immunological
PT   disorders, infections, cell proliferative disorders, microbial
PT   infections -
XX
PS   Claim 4; Page 93; 95pp; English.
XX
CC   This sequence represents the cDNA for a human immune system molecule
CC   (IMOL) isolated as clone 1890540 from the Incyte BLADTUT07 library.
CC   The human IMOLs (AAB15536-B15550) and their encoding polynucleotides
CC   (AAA95775-A95789), and compositions comprising them are useful for the
CC   diagnosis, treatment or prevention of immunological disorders,
CC   infections and cell proliferative disorders, including cancer. The IMOL
CC   may be used to treat or prevent disorders associated with decreased
CC   expression or activity of IMOL, such as immunological disorders
CC   (e.g. inflammation, actinic keratosis, AIDS, Addison's disease),
CC   haematopoietic cancer, infections caused by virus (e.g. adenovirus,
CC   parvovirus, coronavirus), bacteria (e.g. Staphylococcus, Streptococcus,
CC   Shigella), fungi (e.g. Aspergillus, Blastomyces), parasites (e.g.
CC   Plasmodium, Trypanosoma, intestinal protozoa), cell proliferative
CC   disorders (e.g. actinic keratosis, arteriosclerosis, bursitis), and
CC   cancers (e.g. leukemia, melanoma, sarcoma). The peptides are also
CC   useful as immunogens for the development of antibodies that
CC   specifically recognizes these peptides. The polynucleotides may be used
CC   to detect and quantify gene expression in biopsied tissues in which
CC   expression of IMOL may be correlated with the disease, as targets in a
CC   microarray, to detect differences in gene sequences among normal,
CC   carrier and affected individuals, and for screening libraries of
CC   compounds in drug screening techniques. Antibodies which specifically
CC   bind to IMOL may be used for the diagnosis of disorders characterized
CC   by expression of IMOL, or in assays to monitor patients being treated
CC   with IMOL or agonists, antagonists, or inhibitors of IMOL.
XX
SQ   Sequence 1760 BP; 505 A; 376 C; 395 G; 484 T; 0 other;

Alignment Scores:
Pred. No.:                2.02e-99        Length:          1760
Score:                    1367.00         Matches:         246
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       21              Gaps:            0
```

```
US-10-036-041-2 (1-246) x AAA95787 (1-1760)

Qy       1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124 ATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTCCTCCCTTTTTGC 183

Qy      21 LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     184 CTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGT 243

Qy      41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     244 AAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGC 303

Qy      61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     304 CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAA 363

Qy      81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     364 GGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAG 423

Qy     101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     424 CATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTC 483

Qy     121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     484 ATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTT 543

Qy     141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     544 GAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCA 603

Qy     161 GlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluValTyrVal 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     604 GGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTG 663

Qy     181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     664 TACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAA 723

Qy     201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTrpLeu 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     724 TCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTG 783

Qy     221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     784 CGAATGGGCAATGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTC 843

Qy     241 LeuLeuPheGluThrLys 246
           ||||||||||||||||||
Db     844 CTGCTCTTTGAAACTAAG 861

RESULT 6
ABK35590
ID   ABK35590 standard; DNA; 960 BP.
XX
AC   ABK35590;
XX
DT   08-MAY-2002  (first entry)
XX
DE   Gene encoding novel human secreted or membrane-associated protein #9.
XX
KW   Human; secreted protein; membrane-associated protein; hypertension;
KW   inflammatory disorder; neurological disorder; haematopoietic disorder;
KW   skeletal developmental disorder; growth abnormality; autoimmune disorder;
KW   neurodegenerative disorder; nervous system disorder; bacterial infection;
KW   peripheral myelinopathy; viral infection; cancer; obesity; diabetes;
KW   hypotension; sexual development disorder; blood disorder; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200204600-A2.
XX
PD   17-JAN-2002.
XX
PF   12-JUL-2001; 2001WO-US21985.
XX
PR   12-JUL-2000; 2000US-218033P.
PR   21-AUG-2000; 2000US-226517P.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
PA   (GLAX ) GLAXO GROUP LTD.
XX
PI   Agarwal P,  Cogswell JP,  Lai Y,  Martensen SA,  Rizvi SK,  Strum JC;
PI   Smith RF,  Xiang Z,  Xie Q;
XX
DR   WPI; 2002-188468/24.
DR   P-PSDB; AAU84370.
XX
PT   Novel secreted and membrane-associated polypeptides and polynucleotides
PT   encoding the polypeptides, for preventing, treating and ameliorating
PT   cancers, mental or sexual developmental disorders, and malignant tumours
PT   -
XX
PS   Claim 2; Page 106; 151pp; English.
XX
CC   The present invention relates to the isolation of novel human secreted
CC   or membrane-associated proteins and the genes encoding them. The
CC   sequences of the invention are useful for treating, preventing and
CC   ameliorating various diseases such as inflammatory disorders (e.g.
CC   asthma), neurological disorders (e.g. dementia), haematopoietic
CC   disorders, skeletal developmental disorders, growth abnormalities,
CC   neurodegenerative disorders (e.g. Huntington's disease), nervous system
CC   disorders, autoimmune disorders (e.g. rheumatoid arthritis),
CC   peripheral myelinopathies, viral and bacterial infections,
CC   alpha-mannosidosis, diabetes, cancers, malignant tumours, hyper- and
CC   hypotension, obesity, bulimia, anorexia, manic depression, delirium,
CC   mental retardation, Tourette's syndrome, schizophrenia, growth, mental
CC   or sexual development disorders, and dysfunctions of the blood cascade
CC   system including those leading to stroke. ABK35582-ABK35609 represent
CC   the genes encoding the novel human secreted or membrane-associated
CC   proteins of the invention.
XX
SQ   Sequence 960 BP; 261 A; 232 C; 262 G; 205 T; 0 other;

Alignment Scores:
Pred. No.:              4.94e-96        Length:         960
Score:                  1320.50         Matches:        246
Percent Similarity:     77.12%          Conservative:   0
Best Local Similarity:  77.12%          Mismatches:     0
Query Match:            96.60%          Indels:         73
DB:                     24              Gaps:           1

US-10-036-041-2 (1-246) x ABK35590 (1-960)

Qy       1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTCCTCCCTTTTTGC 60

Qy      21 LeuCysGlnAspGluTyrMetGlu---------------------------------- 28
           |||||||||||||||||||||||
Db      61 CTGTGTCAAGATGAATACATGGAGGTGAGCGGAAGAACTAATAAAGTGGTGGCAAGAATA 120

Qy      28 ---------------------------------------------------------- 28

Db     121 GTGCAAAGCCACCAGCAGACTGGCCGTAGCGGCTCCAGGAGGGAGAAAGTGAGAGAGCGG 180

Qy      28 ---------------------------------------------------------- 28

Db     181 AGCCATCCTAAAACTGGGACTGTGGATAATAACACTTCTACAGACCTAAAATCCCTGAGA 240

Qy      28 ---------------------------------------------------------- 28
```

```
Db    241 CCAGATGAGCTACCGCACCCCGAGGTAGATGACCTAGCCCAGATCACCACATTCTGGGGC 300

Qy     29 ---SerProGlnThrGlyGlyLeuProProAspCysSerLysCysCysHisGlyAspTyr 47
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTAC 360

Qy     48 SerPheArgGlyTyrGlnGlyProProGlyProProGlyProProGlyIleProGlyAsn 67
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAAC 420

Qy     68 HisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGluGlyAlaLysGlyGluLysGly 87
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGC 480

Qy     88 AspLysGlyAspLeuGlyProArgGlyGluArgGlyGlnHisGlyProLysGlyGluLys 107
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAG 540

Qy    108 GlyTyrProGlyIleProProGluLeuGlnIleAlaPheMetAlaSerLeuAlaThrHis 127
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCAC 600

Qy    128 PheSerAsnGlnAsnSerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhe 147
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTC 660

Qy    148 PheAspValMetThrGlyArgPheGlyAlaProValSerGlyValTyrPhePheThrPhe 167
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGGTGTGTATTTCTTCACCTTC 720

Qy    168 SerMetMetLysHisGluAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsn 187
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATGGCAAC 780

Qy    188 ThrValPheSerMetTyrSerTyrGluMetLysGlyLysSerAspThrSerSerAsnHis 207
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCAATCAT 840

Qy    208 AlaValLeuLysLeuAlaLysGlyAspGluValTrpLeuArgMetGlyAsnGlyAlaLeu 227
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTC 900

Qy    228 HisGlyAspHisGlnArgPheSerThrPheAlaGlyPheLeuLeuPheGluThrLys 246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTAAG 957

RESULT 7
AAC99776
ID   AAC99776 standard; cDNA; 1035 BP.
XX
AC   AAC99776;
XX
DT   08-MAR-2001  (first entry)
XX
DE   Skin cell cDNA, SEQ ID NO: 424.
XX
KW   Rat; skin cell; cytostatic; antiinflammatory; anti-HIV;
KW   nootropic; neuroprotective; vulnerary; immunomodulatory; vaccine;
KW   keratinocyte growth stimulation; cancer; angiogenesis inhibition;
KW   inflammation; neurological disease; ss.
XX
OS   Rattus sp.
XX
PN   WO200069884-A2.
XX
PD   23-NOV-2000.
XX
PF   15-MAY-2000; 2000WO-NZ00075.
XX
PR   14-MAY-1999;   99US-0312283.
XX
PA   (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI   Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD, Murison JG;
XX
DR   WPI; 2001-007495/01.
DR   P-PSDB; AAB55908.
XX
PT   New isolated polynucleotide used in the identification of genetic
PT   disorders and encoding polypeptides used for treating inflammatory
PT   disease, cancer and neurological diseases -
XX
PS   Claim 1; Page 317-318; 352pp; English.
XX
CC   The present polynucleotide encodes a polypeptide which is expressed in
CC   mammalian skin cells. The polypeptide is useful for stimulating
CC   keratinocyte growth and motility, inhibiting the growth of cancer cells,
CC   modulating angiogenesis, inhibiting angiogenesis and vascularisation of
CC   tumours, modulating skin inflammation, stimulating the growth of
CC   epithelial cells, inhibiting the binding of human immunodeficiency virus
CC   (HIV)-1 to leukocytes, and treating inflammmatory disease, cancer and
CC   neurological diseases. The polynucleotide can be used as a marker, in
CC   the identification of genetic disorders, and for the design of
CC   oligonucleotides for examining expression patterns.
XX
SQ   Sequence 1035 BP; 255 A; 242 C; 298 G; 240 T; 0 other;

Alignment Scores:
Pred. No.:                3.06e-95        Length:          1035
Score:                    1311.00         Matches:         236
Percent Similarity:       97.15%          Conservative:    3
Best Local Similarity:    95.93%          Mismatches:      7
Query Match:              95.90%          Indels:          0
DB:                       22              Gaps:            0

US-10-036-041-2 (1-246) x AAC99776 (1-1035)

Qy      1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys 20
          ||||||   |||||||||:::::|||   ||||||||||||   |||||||||||||||
Db     92 ATGCTCAGGAGGCAGCTCGTCTGGTGGCACCTGCTGGCTTTGCTTTCCTCCCATTTTGC 151

Qy     21 LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40
          |||||||||||||||||||||||||||||||   |||||||||||||||||||||||||
Db    152 CTGTGTCAAGATGAATACATGGAGTCTCCACAAGCTGGAGGACTGCCCCCAGACTGCAGC 211

Qy     41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
          ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db    212 AAGTGTTGCCATGGAGATTATGGATTCCGTGGTTACCAAGGGCCCCCTGGACCCCCAGGT 271

Qy     61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    272 CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGAAATAACGGAGCCACTGGCCACGAA 331

Qy     81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    332 GGGGCCAAGGGTGAGAAAGGAGACAAAGGCGACCTGGGGCCTCGAGGGGAACGGGGGCAG 391

Qy    101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe 120
          ||||||||||||||   ||||||||||||:::|||||||||||||||||||||||||||
Db    392 CATGGCCCCAAAGGATAGAAGGGATACCCAGGGGTGCCACCAGAGCTGCAGATTGCGTTC 451

Qy    121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    452 ATGGCTTCTCTAGCGACTCACTTCAGCAATCAGAACAGTGGCATTATCTTCAGCAGTGTT 511

Qy    141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    512 GAGACCAACATTGGAAACTTCTTCGATGTCATGACTGGTAGATTTGGGGCCCCCGTATCA 571

Qy    161 GlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluValTyrVal 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    572 GGCGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGACGTGGAGGAAGTGTATGTG 631

Qy    181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200
          |||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
```

```
Db    632 TACCTTATGCACAATGGTAACACGGTGTTCAGCATGTACAGCTATGAAACAAAGGGAAAA 691

Qy    201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTrpLeu 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    692 TCAGATACATCCAGCAACCATGCAGTGCTGAAGTTGGCCAAAGGAGATGAAGTCTGGCTA 751

Qy    221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    752 AGAATGGGCAACGGTGCCCTCCATGGGGACCACCAGCGCTTCTCTACCTTCGCAGGCTTT 811

Qy    241 LeuLeuPheGluThrLys 246
          ||||||||||||||||||
Db    812 CTGCTTTTTGAAACTAAG 829

RESULT 8
ABL34928
ID   ABL34928 standard; cDNA; 1035 BP.
XX
AC   ABL34928;
XX
DT   04-APR-2002  (first entry)
XX
DE   Rat cDNA isolated from skin cells SEQ ID NO: 424.
XX
KW   Human; rat; mouse; skin cell; skin wound; cancer; growth defect;
KW   developmental defect; inflammatory disease; dermatological; vulnerary;
KW   immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene;
KW   ss.
XX
OS   Rattus sp.
XX
PN   WO200190357-A1.
XX
PD   29-NOV-2001.
XX
PF   24-MAY-2001; 2001WO-NZ00099.
XX
PR   24-MAY-2000; 2000US-206650P.
PR   25-JUL-2000; 2000US-221232P.
XX
PA   (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI   Watson JD,  Strachan L,  Sleeman M,  Onrust R,  Murison JG,  Kumble KD;
XX
DR   WPI; 2002-122020/16.
XX
PT   New polynucleotides and polypeptides encoded by the polynucleotides
PT   isolated from skin cells, useful for treating skin wounds, cancers,
PT   growth and developmental defects, inflammatory diseases, or for
PT   modulating immune responses
XX
PS   Claim 1; Page 262; 466pp; English.
XX
CC   The present invention provides the protein and coding sequences of cDNAs
CC   isolated from human, murine and rat skin cell libraries. The sequences
CC   can be used in the development of therapeutic agents useful in the
CC   treatment of skin diseases, including skin wounds, cancer, growth
CC   defects, developmental defects and inflammatory diseases. The proteins
CC   have important roles in the induction of hair growth, cell proliferation
CC   and cell-cell interaction, in maintaining tissue integrity, in wound
CC   healing and in modulating immune responses. The present sequence is a
CC   cDNA of the invention.
XX
SQ   Sequence 1035 BP; 255 A; 242 C; 298 G; 240 T; 0 other;

Alignment Scores:
Pred. No.:              3.06e-95        Length:         1035
Score:                  1311.00         Matches:        236
Percent Similarity:     97.15%          Conservative:   3
Best Local Similarity:  95.93%          Mismatches:     7
Query Match:            95.90%          Indels:         0
DB:                     24              Gaps:           0

US-10-036-041-2 (1-246) x ABL34928 (1-1035)

Qy      1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys 20
          ||||||   |||||||||:::::|||   ||||||||||||   ||||||||||||||||
Db     92 ATGCTCAGGAGGCAGCTCGTCTGGTGGCACCTGCTGGCTTTGCTTTCCTCCCATTTTGC 151

Qy     21 LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40
          ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db    152 CTGTGTCAAGATGAATACATGGAGTCTCCACAAGCTGGAGGACTGCCCCCAGACTGCAGC 211

Qy     41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
          ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db    212 AAGTGTTGCCATGGAGATTATGGATTCCGTGGTTACCAAGGGCCCCCTGGACCCCCAGGT 271

Qy     61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    272 CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGAAATAACGGAGCCACTGGCCACGAA 331

Qy     81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    332 GGGGCCAAGGGTGAGAAAGGAGACAAAGGCGACCTGGGGCCTCGAGGGGAACGGGGGCAG 391

Qy    101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe 120
          ||||||||||||||   ||||||||||||||:::|||||||||||||||||||||||||
Db    392 CATGGCCCCAAAGGATAGAAGGGATACCCAGGGGTGCCACCAGAGCTGCAGATTGCGTTC 451

Qy    121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    452 ATGGCTTCTCTAGCGACTCACTTCAGCAATCAGAACAGTGGCATTATCTTCAGCAGTGTT 511

Qy    141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    512 GAGACCAACATTGGAAACTTCTTCGATGTCATGACTGGTAGATTTGGGGCCCCCGTATCA 571

Qy    161 GlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluValTyrVal 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    572 GGCGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGACGTGGAGGAAGTGTATGTG 631

Qy    181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200
          ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db    632 TACCTTATGCACAATGGTAACACGGTGTTCAGCATGTACAGCTATGAAACAAAGGGAAAA 691

Qy    201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTrpLeu 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    692 TCAGATACATCCAGCAACCATGCAGTGCTGAAGTTGGCCAAAGGAGATGAAGTCTGGCTA 751

Qy    221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    752 AGAATGGGCAACGGTGCCCTCCATGGGGACCACCAGCGCTTCTCTACCTTCGCAGGCTTT 811

Qy    241 LeuLeuPheGluThrLys 246
          ||||||||||||||||||
Db    812 CTGCTTTTTGAAACTAAG 829

RESULT 9
AAC64064
ID   AAC64064 standard; DNA; 1117 BP.
XX
AC   AAC64064;
XX
DT   19-FEB-2001  (first entry)
XX
DE   Mouse zacrp2 DNA, SEQ ID NO:11.
XX
KW   Mouse zacrp2; adipocyte complement related protein homologue;
KW   ACRP30; C1q domain; collagen-like domain; energy balance modulation;
KW   cellular metabolism; metabolic disorder; obesity; anorexia;
KW   antimicrobial agent; infection; platelet aggregation inhibition;
KW   adhesion; activation; vascular injury; antibacterial; antiviral;
KW   human zacrp3 homologue; ds.
XX
OS   Mus musculus.
XX
```

```
PN   WO200063377-A1.
XX
PD   26-OCT-2000.
XX
PF   19-APR-2000; 2000WO-US10454.
XX
PR   20-APR-1999;   99US-0294943.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Piddington CS,  Bishop PD;
XX
DR   WPI; 2000-665243/64.
DR   P-PSDB; AAB29582.
XX
PT   Novel zacrp3 polypeptides used to treat or prevent bacterial or viral
PT   infections, for wound healing, improving blood flow, and to analyze
PT   energy efficiency in mammals -
XX
PS   Disclosure; Page 115-117; 123pp; English.
XX
CC   The invention relates to the human zacrp3 protein (AAB29580) and to
CC   nucleic acids which encode it (AAC64058, AAC64063). Zacrp3 is a homogue
CC   of adipocyte complement related protein (ACRP30) and contains a
CC   collagen-like domain comprising Gly-Xaa-Xaa or Gly-Xaa-Pro repeats, and a
CC   C-terminal C1q domain comprising 10 beta-strands. The zacrp3 gene is
CC   located on chromosome 5p12. The invention also relates to zacrp3
CC   fragments, fusion proteins containing zacrp3 polypeptides,
CC   zacrp3-specific antibodies, expression constructs and host cells
CC   comprising zacrp3 nucleic acids, and methods of recombinant production of
CC   zacrp3. Human zacrp3, and its agonists and antagonists may be used in the
CC   study and modulation of cellular metabolism and energy balance in
CC   mammals, and may therefore be used to treat disorders such as obesity and
CC   anorexia, and conditions associated with these disorders. Due to its C1q
CC   like domain, zacrp3 and zacrp3-containing fusion proteins may be useful
CC   as antimicrobial agents, promoting lysis or phagocytosis of infectious
CC   organisms such as bacteria or viruses. Zacrp3, its fragments, fusion
CC   proteins, antibodies and activity modulators may also be used to inhibit
CC   collagen-induced platelet aggregation, adhesion, or activation, and may
CC   therefore have potential for promoting blood flow within the vasculature
CC   of a mammal e.g., to treat injury to the vasculature or other collagenous
CC   tissue. Human zacrp3 and its antibodies may additionally be used to study
CC   dimerisation and oligomerisation. The present sequence represents DNA
CC   encoding mouse zacrp2, a homologue of human zacrp3.
XX
SQ   Sequence 1117 BP; 284 A; 272 C; 293 G; 268 T; 0 other;

Alignment Scores:
Pred. No.:              3.34e-95      Length:         1117
Score:                  1311.00       Matches:        236
Percent Similarity:     96.75%        Conservative:   2
Best Local Similarity:  95.93%        Mismatches:     8
Query Match:            95.90%        Indels:         0
DB:                     21            Gaps:           0

US-10-036-041-2 (1-246) x AAC64064 (1-1117)

Qy       1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys 20
           ||||||   ||||||   |||:::|||   ||||||   |||   ||||||||||||||||
Db     111 ATGCTCGGGAGGCAGCGCATCTGGTGGCACCTGCTGCCTTTGCTTTTCCTCCCATTTTGC 170

Qy      21 LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40
           ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db     171 CTGTGTCAAGATGAATACATGGAGTCTCCACAAGCTGGAGGACTGCCCCCAGACTGCAGC 230

Qy      41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
           ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db     231 AAGTGTTGCCATGGAGATTATGGATTTCGTGGTTACCAAGGGCCCCCTGGACCTCCAGGT 290

Qy      61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     291 CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGGAACAATGGAGCTACTGGCCATGAA 350

Qy      81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     351 GGGGCCAAAGGTGAGAAAGGAGACAAAGGCGACCTAGGCCCTCGAGGAGAACGGGGGCAG 410

Qy     101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe 120
           ||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||
Db     411 CATGGCCCCAAAGGAGAGAAAGGCTACCCAGGGGTGCCACCAGAACTGCAGATTGCATTC 470

Qy     121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     471 ATGGCTTCTCTAGCAACTCACTTCAGCAATCAGAACAGTGGCATTATCTTCAGCAGTGTT 530

Qy     141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     531 GAGACCAACATTGGAAACTTCTTCGATGTCATGACTGGGAGATTTGGGGCCCCCGTATCA 590

Qy     161 GlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluValTyrVal 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     591 GGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGACGTAGAGGAAGTGTATGTG 650

Qy     181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200
           ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db     651 TACCTTATGCACAACGGCAACACAGTCTTCAGCATGTACAGCTATGAAACAAAGGGAAAA 710

Qy     201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTrpLeu 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     711 TCAGATACATCCAGCAACCATGCAGTGCTGAAGTTGGCCAAAGGAGATGAAGTCTGGCTA 770

Qy     221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     771 AGAATGGGCAACGGTGCCCTCCACGGGGACCACCAGCGCTTCTCCACCTTCGCAGGCTTT 830

Qy     241 LeuLeuPheGluThrLys 246
           ||||||||||||||||||
Db     831 CTGCTCTTTGAAACTAAG 848

RESULT 10
AAZ61633
ID   AAZ61633 standard; cDNA; 1123 BP.
XX
AC   AAZ61633;
XX
DT   27-MAR-2000  (first entry)
XX
DE   cDNA encoding rat skin cell secreted protein, SEQ ID NO:28.
XX
KW   Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast;
KW   embryonic skin cell; keratinocyte stem cell; transit amplifying cell;
KW   secreted; transmembrane; inflammation; cancer; neurological disease;
KW   angiogenesis; tumour vascularisation; growth disorder;
KW   developmental disorder; skin wound; hair follicle disorder;
KW   anti-inflammatory; cytostatic; neuroprotective; vulnery; ss.
XX
OS   Rattus sp.
XX
PN   WO9955865-A1.
XX
PD   04-NOV-1999.
XX
PF   29-APR-1999;   99WO-NZ00051.
XX
PR   29-APR-1998;   98US-0069726.
PR   09-NOV-1998;   98US-0188930.
XX
PA   (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI   Strachan L,  Sleeman M,  Watson JD,  Onrust R,  Kumble A,  Murison JG;
XX
DR   WPI; 2000-072177/06.
XX
PT   Novel polynucleotides useful for the treatment of various conditions
PT   including wounds and cancer -
XX
```

```
PS   Claim 1; Page 73; 235pp; English.
XX
CC   The invention relates to novel nucleic acid sequences derived from rat
CC   dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,
CC   and mouse embryonic skin, keratinocyte stem cells and transit amplifying
CC   cells. Polypeptides of the invention may be used to treat inflammation,
CC   cancer and neurological diseases. The proteins may be used to stimulate
CC   the growth and motility of keratinocytes, to inhibit the growth of
CC   cancer cells, to modulate angiogenesis and tumour vascularisation, to
CC   modulate skin inflammation, to modulate epithelial cell growth and to
CC   inhibit binding of HIV-1 to leukocytes. The invention may also be used
CC   to treat growth and developmental defects, skin wounds and hair follicle
CC   disorders. Sequences AAZ61606-Z61832 represent cDNA sequences derived
CC   from several mouse, rat or human skin cell types. Sequences
CC   AAZ61606-Z61649, AAZ61725-Z61765, AAZ61802-Z61811 and AAZ61826 encode
CC   proteins with an N-terminal signal sequence, indicating that the proteins
CC   are secreted. Sequences AAZ61650-Z61668, AAZ61766-Z61780, AAZ61812-Z61817
CC   and AAZ61827-Z61829 encode proteins with one or more putative
CC   transmembrane domains.
XX
SQ   Sequence 1123 BP; 277 A; 266 C; 321 G; 258 T; 1 other;

Alignment Scores:
Pred. No.:              3.36e-95        Length:         1123
Score:                  1311.00         Matches:        236
Percent Similarity:     97.15%          Conservative:   3
Best Local Similarity:  95.93%          Mismatches:     7
Query Match:            95.90%          Indels:         0
DB:                     21              Gaps:           0

US-10-036-041-2 (1-246) x AAZ61633 (1-1123)

Qy       1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys 20
           ||||||  |||||||||:::::|||  ||||||||||||  ||||||||||||||||
Db     180 ATGCTCAGGAGGCAGCTCGTCTGGTGGCACCTGCTGGCTTTGCTTTTCCTCCCATTTTGC 239

Qy      21 LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40
           ||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db     240 CTGTGTCAAGATGAATACATGGAGTCTCCACAAGCTGGAGGACTGCCCCCAGACTGCAGC 299

Qy      41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
           ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db     300 AAGTGTTGCCATGGAGATTATGGATTCCGTGGTTACCAAGGGCCCCCTGGACCCCCAGGT 359

Qy      61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     360 CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGAAATAACGGAGCCACTGGCCACGAA 419

Qy      81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     420 GGGGCCAAGGGTGAGAAAGGAGACAAAGGCGACCTGGGGCCTCGAGGGGAACGGGGGCAG 479

Qy     101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe 120
           ||||||||||||||  ||||||||||||||:::||||||||||||||||||||||||||
Db     480 CATGGCCCCAAAGGATAGAAGGGATACCCAGGGGTGCCACCAGAGCTGCAGATTGCGTTC 539

Qy     121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     540 ATGGCTTCTCTAGCGACTCACTTCAGCAATCAGAACAGTGGCATTATCTTCAGCAGTGTT 599

Qy     141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     600 GAGACCAACATTGGAAACTTCTTCGATGTCATGACTGGTAGATTTGGGGCCCCCGTATCA 659

Qy     161 GlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluValTyrVal 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     660 GGCGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGACGTGGAGGAAGTGTATGTG 719

Qy     181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200
           ||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db     720 TACCTTATGCACAATGGTAACACGGTGTTCAGCATGTACAGCTATGAAACAAAGGGAAAA 779

Qy     201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTrpLeu 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     780 TCAGATACATCCAGCAACCATGCAGTGCTGAAGTTGGCCAAAGGAGATGAAGTCTGGCTA 839

Qy     221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     840 AGAATGGGCAACGGTGCCCTCCATGGGGACCACCAGCGCTTCTCTACCTTCGCAGGCTTT 899

Qy     241 LeuLeuPheGluThrLys 246
           ||||||||||||||||||
Db     900 CTGCTTTTTGAAACTAAG 917

RESULT 11
AAZ61730
ID   AAZ61730 standard; cDNA; 1123 BP.
XX
AC   AAZ61730;
XX
DT   27-MAR-2000  (first entry)
XX
DE   cDNA encoding rat skin cell secreted protein, SEQ ID NO:203.
XX
KW   Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast;
KW   embryonic skin cell; keratinocyte stem cell; transit amplifying cell;
KW   secreted; transmembrane; inflammation; cancer; neurological disease;
KW   angiogenesis; tumour vascularisation; growth disorder;
KW   developmental disorder; skin wound; hair follicle disorder;
KW   anti-inflammatory; cytostatic; neuroprotective; vulnery; ss.
XX
OS   Rattus sp.
XX
PN   WO9955865-A1.
XX
PD   04-NOV-1999.
XX
PF   29-APR-1999;   99WO-NZ000051.
XX
PR   29-APR-1998;   98US-0069726.
PR   09-NOV-1998;   98US-0188930.
XX
PA   (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI   Strachan L, Sleeman M, Watson JD, Onrust R, Kumble A, Murison JG;
XX
DR   WPI; 2000-072177/06.
DR   P-PSDB; AAY76025.
XX
PT   Novel polynucleotides useful for the treatment of various conditions
PT   including wounds and cancer -
XX
PS   Claim 1; Page 137; 235pp; English.
XX
CC   The invention relates to novel nucleic acid sequences derived from rat
CC   dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,
CC   and mouse embryonic skin, keratinocyte stem cells and transit amplifying
CC   cells. Polypeptides of the invention may be used to treat inflammation,
CC   cancer and neurological diseases. The proteins may be used to stimulate
CC   the growth and motility of keratinocytes, to inhibit the growth of
CC   cancer cells, to modulate angiogenesis and tumour vascularisation, to
CC   modulate skin inflammation, to modulate epithelial cell growth and to
CC   inhibit binding of HIV-1 to leukocytes. The invention may also be used
CC   to treat growth and developmental defects, skin wounds and hair follicle
CC   disorders. Sequences AAZ61606-Z61832 represent cDNA sequences derived
CC   from several mouse, rat or human skin cell types. Sequences
CC   AAZ61606-Z61649, AAZ61725-Z61765, AAZ61802-Z61811 and AAZ61826 encode
CC   proteins with an N-terminal signal sequence, indicating that the proteins
CC   are secreted. Sequences AAZ61650-Z61668, AAZ61766-Z61780, AAZ61812-Z61817
CC   and AAZ61827-Z61829 encode proteins with one or more putative
CC   transmembrane domains.
XX
SQ   Sequence 1123 BP; 277 A; 266 C; 321 G; 258 T; 1 other;

Alignment Scores:
Pred. No.:              3.36e-95        Length:         1123
```

| | | | |
|---|---|---|---|
| Score: | 1311.00 | Matches: | 236 |
| Percent Similarity: | 97.15% | Conservative: | 3 |
| Best Local Similarity: | 95.93% | Mismatches: | 7 |
| Query Match: | 95.90% | Indels: | 0 |
| DB: | 21 | Gaps: | 0 |

US-10-036-041-2 (1-246) x AAZ61730 (1-1123)

```
Qy       1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys 20
           ||||||   |||||||||:::::|||   ||||||||||||   ||||||||||||||||
Db     180 ATGCTCAGGAGGCAGCTCGTCTGGTGGCACCTGCTGGCTTTGCTTTTCCTCCCATTTTGC 239

Qy      21 LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40
           ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db     240 CTGTGTCAAGATGAATACATGGAGTCTCCACAAGCTGGAGGACTGCCCCCAGACTGCAGC 299

Qy      41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
           ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db     300 AAGTGTTGCCATGGAGATTATGGATTCCGTGGTTACCAAGGGCCCCCTGGACCCCCAGGT 359

Qy      61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     360 CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGAAATAACGGAGCCACTGGCCACGAA 419

Qy      81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     420 GGGGCCAAGGGTGAGAAAGGAGACAAAGGCGACCTGGGGCCTCGAGGGGAACGGGGGCAG 479

Qy     101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe 120
           ||||||||||||||   ||||||||||||||:::||||||||||||||||||||||||||
Db     480 CATGGCCCCAAAGGATAGAAGGGATACCCAGGGGTGCCACCAGAGCTGCAGATTGCGTTC 539

Qy     121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     540 ATGGCTTCTCTAGCGACTCACTTCAGCAATCAGAACAGTGGCATTATCTTCAGCAGTGTT 599

Qy     141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     600 GAGACCAACATTGGAAACTTCTTCGATGTCATGACTGGTAGATTTGGGGCCCCCGTATCA 659

Qy     161 GlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluValTyrVal 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     660 GGCGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGACGTGGAGGAAGTGTATGTG 719

Qy     181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200
           ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db     720 TACCTTATGCACAATGGTAACACGGTGTTCAGCATGTACAGCTATGAAACAAAGGGAAAA 779

Qy     201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTrpLeu 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     780 TCAGATACATCCAGCAACCATGCAGTGCTGAAGTTGGCCAAAGGAGATGAAGTCTGGCTA 839

Qy     221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     840 AGAATGGGCAACGGTGCCCTCCATGGGGACCACCAGCGCTTCTCTACCTTCGCAGGCTTT 899

Qy     241 LeuLeuPheGluThrLys 246
           ||||||||||||||||||
Db     900 CTGCTTTTTGAAACTAAG 917
```

RESULT 12
AAC99566
ID AAC99566 standard; cDNA; 1123 BP.
XX
AC AAC99566;
XX
DT 08-MAR-2001 (first entry)
XX
DE Skin cell cDNA, SEQ ID NO: 28.
XX
KW Rat; skin cell; cytostatic; antiinflammatory; anti-HIV;
KW nootropic; neuroprotective; vulnerary; immunomodulatory; vaccine;
KW keratinocyte growth stimulation; cancer; angiogenesis inhibition;
KW inflammation; neurological disease; ss.
XX
OS Rattus sp.
XX
PN WO200069884-A2.
XX
PD 23-NOV-2000.
XX
PF 15-MAY-2000; 2000WO-NZ00075.
XX
PR 14-MAY-1999; 99US-0312283.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD, Murison JG;
XX
DR WPI; 2001-007495/01.
DR P-PSDB; AAB55908.
XX
PT New isolated polynucleotide used in the identification of genetic
PT disorders and encoding polypeptides used for treating inflammatory
PT disease, cancer and neurological diseases -
XX
PS Claim 1; Page 87; 352pp; English.
XX
CC The present polynucleotide encodes a polypeptide which is expressed in
CC mammalian skin cells. The polypeptide is useful for stimulating
CC keratinocyte growth and motility, inhibiting the growth of cancer cells,
CC modulating angiogenesis, inhibiting angiogenesis and vascularisation of
CC tumours, modulating skin inflammation, stimulating the growth of
CC epithelial cells, inhibiting the binding of human immunodeficiency virus
CC (HIV)-1 to leukocytes, and treating inflammmatory disease, cancer and
CC neurological diseases. The polynucleotide can be used as a marker, in
CC the identification of genetic disorders, and for the design of
CC oligonucleotides for examining expression patterns.
XX
SQ Sequence 1123 BP; 277 A; 266 C; 321 G; 258 T; 1 other;

| | | | |
|---|---|---|---|
| Alignment Scores: | | | |
| Pred. No.: | 3.36e-95 | Length: | 1123 |
| Score: | 1311.00 | Matches: | 236 |
| Percent Similarity: | 97.15% | Conservative: | 3 |
| Best Local Similarity: | 95.93% | Mismatches: | 7 |
| Query Match: | 95.90% | Indels: | 0 |
| DB: | 22 | Gaps: | 0 |

US-10-036-041-2 (1-246) x AAC99566 (1-1123)

```
Qy       1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys 20
           ||||||   |||||||||:::::|||   ||||||||||||   ||||||||||||||||
Db     180 ATGCTCAGGAGGCAGCTCGTCTGGTGGCACCTGCTGGCTTTGCTTTTCCTCCCATTTTGC 239

Qy      21 LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40
           ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db     240 CTGTGTCAAGATGAATACATGGAGTCTCCACAAGCTGGAGGACTGCCCCCAGACTGCAGC 299

Qy      41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
           ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db     300 AAGTGTTGCCATGGAGATTATGGATTCCGTGGTTACCAAGGGCCCCCTGGACCCCCAGGT 359

Qy      61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     360 CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGAAATAACGGAGCCACTGGCCACGAA 419

Qy      81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     420 GGGGCCAAGGGTGAGAAAGGAGACAAAGGCGACCTGGGGCCTCGAGGGGAACGGGGGCAG 479

Qy     101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe 120
           ||||||||||||||   ||||||||||||||:::||||||||||||||||||||||||||
Db     480 CATGGCCCCAAAGGATAGAAGGGATACCCAGGGGTGCCACCAGAGCTGCAGATTGCGTTC 539

Qy     121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
```

```
Db    540 ATGGCTTCTCTAGCGACTCACTTCAGCAATCAGAACAGTGGCATTATCTTCAGCAGTGTT 599

Qy    141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
Db    600 GAGACCAACATTGGAAACTTCTTCGATGTCATGACTGGTAGATTTGGGGCCCCCGTATCA 659

Qy    161 GlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluValTyrVal 180
Db    660 GGCGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGACGTGGAGGAAGTGTATGTG 719

Qy    181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200
Db    720 TACCTTATGCACAATGGTAACACGGTGTTCAGCATGTACAGCTATGAAACAAAGGGAAAA 779

Qy    201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTrpLeu 220
Db    780 TCAGATACATCCAGCAACCATGCAGTGCTGAAGTTGGCCAAAGGAGATGAAGTCTGGCTA 839

Qy    221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
Db    840 AGAATGGGCAACGGTGCCCTCCATGGGGACCACCAGCGCTTCTCTACCTTCGCAGGCTTT 899

Qy    241 LeuLeuPheGluThrLys 246
Db    900 CTGCTTTTTGAAACTAAG 917

RESULT 13
AAC99663
ID   AAC99663 standard; cDNA; 1123 BP.
XX
AC   AAC99663;
XX
DT   08-MAR-2001  (first entry)
XX
DE   Skin cell cDNA, SEQ ID NO: 203.
XX
KW   Rat; skin cell; cytostatic; antiinflammatory; anti-HIV;
KW   nootropic; neuroprotective; vulnerary; immunomodulatory; vaccine;
KW   keratinocyte growth stimulation; cancer; angiogenesis inhibition;
KW   inflammation; neurological disease; ss.
XX
OS   Rattus sp.
XX
PN   WO200069884-A2.
XX
PD   23-NOV-2000.
XX
PF   15-MAY-2000; 2000WO-NZ00075.
XX
PR   14-MAY-1999;   99US-0312283.
XX
PA   (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI   Watson JD,  Strachan L,  Onrust R,  Sleeman M,  Kumble KD,  Murison JG;
XX
DR   WPI; 2001-007495/01.
DR   P-PSDB; AAB55958.
XX
PT   New isolated polynucleotide used in the identification of genetic
PT   disorders and encoding polypeptides used for treating inflammatory
PT   disease, cancer and neurological diseases -
XX
PS   Claim 1; Page 176-177; 352pp; English.
XX
CC   The present polynucleotide encodes a polypeptide which is expressed in
CC   mammalian skin cells. The polypeptide is useful for stimulating
CC   keratinocyte growth and motility, inhibiting the growth of cancer cells,
CC   modulating angiogenesis, inhibiting angiogenesis and vascularisation of
CC   tumours, modulating skin inflammation, stimulating the growth of
CC   epithelial cells, inhibiting the binding of human immunodeficiency virus
CC   (HIV)-1 to leukocytes, and treating inflammmatory disease, cancer and
CC   neurological diseases. The polynucleotide can be used as a marker, in
CC   the identification of genetic disorders, and for the design of
CC   oligonucleotides for examining expression patterns.
XX
SQ   Sequence 1123 BP; 277 A; 266 C; 321 G; 258 T; 1 other;

Alignment Scores:
Pred. No.:                3.36e-95      Length:          1123
Score:                    1311.00       Matches:         236
Percent Similarity:       97.15%        Conservative:    3
Best Local Similarity:    95.93%        Mismatches:      7
Query Match:              95.90%        Indels:          0
DB:                       22            Gaps:            0

US-10-036-041-2 (1-246) x AAC99663 (1-1123)

Qy      1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys 20
Db    180 ATGCTCAGGAGGCAGCTCGTCTGGTGGCACCTGCTGGCTTTGCTTTTCCTCCCATTTTGC 239

Qy     21 LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40
Db    240 CTGTGTCAAGATGAATACATGGAGTCTCCACAAGCTGGAGGACTGCCCCCAGACTGCAGC 299

Qy     41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
Db    300 AAGTGTTGCCATGGAGATTATGGATTCCGTGGTTACCAAGGGCCCCCTGGACCCCCAGGT 359

Qy     61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
Db    360 CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGAAATAACGGAGCCACTGGCCACGAA 419

Qy     81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100
Db    420 GGGGCCAAGGGTGAGAAAGGAGACAAAGGCGACCTGGGGCCTCGAGGGGAACGGGGGCAG 479

Qy    101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe 120
Db    480 CATGGCCCCAAAGGATAGAAGGGATACCCAGGGGTGCCACCAGAGCTGCAGATTGCGTTC 539

Qy    121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
Db    540 ATGGCTTCTCTAGCGACTCACTTCAGCAATCAGAACAGTGGCATTATCTTCAGCAGTGTT 599

Qy    141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
Db    600 GAGACCAACATTGGAAACTTCTTCGATGTCATGACTGGTAGATTTGGGGCCCCCGTATCA 659

Qy    161 GlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluValTyrVal 180
Db    660 GGCGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGACGTGGAGGAAGTGTATGTG 719

Qy    181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200
Db    720 TACCTTATGCACAATGGTAACACGGTGTTCAGCATGTACAGCTATGAAACAAAGGGAAAA 779

Qy    201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTrpLeu 220
Db    780 TCAGATACATCCAGCAACCATGCAGTGCTGAAGTTGGCCAAAGGAGATGAAGTCTGGCTA 839

Qy    221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
Db    840 AGAATGGGCAACGGTGCCCTCCATGGGGACCACCAGCGCTTCTCTACCTTCGCAGGCTTT 899

Qy    241 LeuLeuPheGluThrLys 246
Db    900 CTGCTTTTTGAAACTAAG 917

RESULT 14
ABL34718
ID   ABL34718 standard; cDNA; 1123 BP.
XX
AC   ABL34718;
XX
```

```
DT   04-APR-2002  (first entry)
XX
DE   Rat cDNA isolated from skin cells SEQ ID NO: 28.
XX
KW   Human; rat; mouse; skin cell; skin wound; cancer; growth defect;
KW   developmental defect; inflammatory disease; dermatological; vulnerary;
KW   immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene;
KW   ss.
XX
OS   Rattus sp.
XX
PN   WO200190357-A1.
XX
PD   29-NOV-2001.
XX
PF   24-MAY-2001; 2001WO-NZ00099.
XX
PR   24-MAY-2000; 2000US-206650P.
PR   25-JUL-2000; 2000US-221232P.
XX
PA   (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI   Watson JD,  Strachan L,  Sleeman M,  Onrust R,  Murison JG,  Kumble KD;
XX
DR   WPI; 2002-122020/16.
XX
PT   New polynucleotides and polypeptides encoded by the polynucleotides
PT   isolated from skin cells, useful for treating skin wounds, cancers,
PT   growth and developmental defects, inflammatory diseases, or for
PT   modulating immune responses  -
XX
PS   Claim 1; Page 86-87; 466pp; English.
XX
CC   The present invention provides the protein and coding sequences of cDNAs
CC   isolated from human, murine and rat skin cell libraries. The sequences
CC   can be used in the development of therapeutic agents useful in the
CC   treatment of skin diseases, including skin wounds, cancer, growth
CC   defects, developmental defects and inflammatory diseases. The proteins
CC   have important roles in the induction of hair growth, cell proliferation
CC   and cell-cell interaction, in maintaining tissue integrity, in wound
CC   healing and in modulating immune responses. The present sequence is a
CC   cDNA of the invention.
XX
SQ   Sequence 1123 BP; 277 A; 266 C; 321 G; 258 T; 1 other;

Alignment Scores:
Pred. No.:              3.36e-95        Length:         1123
Score:                  1311.00         Matches:        236
Percent Similarity:     97.15%          Conservative:   3
Best Local Similarity:  95.93%          Mismatches:     7
Query Match:            95.90%          Indels:         0
DB:                     24              Gaps:           0

US-10-036-041-2 (1-246) x ABL34718 (1-1123)

Qy       1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheGys 20
           ||||||   |||||||||:::::|||   ||||||||||||   ||||||||||||||||
Db     180 ATGCTCAGGAGGCAGCTCGTCTGGTGGCACCTGCTGGCTTTGCTTTTCCTCCCATTTTGC 239

Qy      21 LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40
           ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db     240 CTGTGTCAAGATGAATACATGGAGTCTCCACAAGCTGGAGGACTGCCCCCAGACTGCAGC 299

Qy      41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
           ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db     300 AAGTGTTGCCATGGAGATTATGGATTCCGTGGTTACCAAGGGCCCCCTGGACCCCCAGGT 359

Qy      61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     360 CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGAAATAACGGAGCCACTGGCCACGAA 419

Qy      81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     420 GGGGCCAAGGGTGAGAAAGGAGACAAAGGCGACCTGGGGCCTCGAGGGGAACGGGGGCAG 479

Qy     101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe 120
           ||||||||||||||   ||||||||||||||:::||||||||||||||||||||||||||
Db     480 CATGGCCCCAAAGGATAGAAGGGATACCCAGGGGTGCCACCAGAGCTGCAGATTGCGTTC 539

Qy     121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     540 ATGGCTTCTCTAGCGACTCACTTCAGCAATCAGAACAGTGGCATTATCTTCAGCAGTGTT 599

Qy     141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     600 GAGACCAACATTGGAAACTTCTTCGATGTCATGACTGGTAGATTTGGGGCCCCCGTATCA 659

Qy     161 GlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluValTyrVal 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     660 GGCGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGACGTGGAGGAAGTGTATGTG 719

Qy     181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200
           ||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db     720 TACCTTATGCACAATGGTAACACGGTGTTCAGCATGTACAGCTATGAAACAAAGGGAAAA 779

Qy     201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTrpLeu 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     780 TCAGATACATCCAGCAACCATGCAGTGCTGAAGTTGGCCAAAGGAGATGAAGTCTGGCTA 839

Qy     221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     840 AGAATGGGCAACGGTGCCCTCCATGGGGACCACCAGCGCTTCTCTACCTTCGCAGGCTTT 899

Qy     241 LeuLeuPheGluThrLys 246
           ||||||||||||||||||
Db     900 CTGCTTTTTGAAACTAAG 917

RESULT 15
ABL34815
ID   ABL34815 standard; cDNA; 1123 BP.
XX
AC   ABL34815;
XX
DT   04-APR-2002  (first entry)
XX
DE   Rat cDNA isolated from skin cells SEQ ID NO: 203.
XX
KW   Human; rat; mouse; skin cell; skin wound; cancer; growth defect;
KW   developmental defect; inflammatory disease; dermatological; vulnerary;
KW   immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene;
KW   ss.
XX
OS   Rattus sp.
XX
PN   WO200190357-A1.
XX
PD   29-NOV-2001.
XX
PF   24-MAY-2001; 2001WO-NZ00099.
XX
PR   24-MAY-2000; 2000US-206650P.
PR   25-JUL-2000; 2000US-221232P.
XX
PA   (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI   Watson JD,  Strachan L,  Sleeman M,  Onrust R,  Murison JG,  Kumble KD;
XX
DR   WPI; 2002-122020/16.
XX
PT   New polynucleotides and polypeptides encoded by the polynucleotides
PT   isolated from skin cells, useful for treating skin wounds, cancers,
PT   growth and developmental defects, inflammatory diseases, or for
PT   modulating immune responses  -
XX
PS   Claim 1; Page 155-156; 466pp; English.
XX
```

```
CC   The present invention provides the protein and coding sequences of cDNAs
CC   isolated from human, murine and rat skin cell libraries. The sequences
CC   can be used in the development of therapeutic agents useful in the
CC   treatment of skin diseases, including skin wounds, cancer, growth
CC   defects, developmental defects and inflammatory diseases. The proteins
CC   have important roles in the induction of hair growth, cell proliferation
CC   and cell-cell interaction, in maintaining tissue integrity, in wound
CC   healing and in modulating immune responses. The present sequence is a
CC   cDNA of the invention.
XX
SQ   Sequence 1123 BP; 277 A; 266 C; 321 G; 258 T; 1 other;

Alignment Scores:
Pred. No.:              3.36e-95        Length:         1123
Score:                  1311.00         Matches:        236
Percent Similarity:     97.15%          Conservative:   3
Best Local Similarity:  95.93%          Mismatches:     7
Query Match:            95.90%          Indels:         0
DB:                     24              Gaps:           0

US-10-036-041-2 (1-246) x ABL34815 (1-1123)

Qy       1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys 20
           ||||||   |||||||||:::::|||   ||||||||||||   ||||||||||||||||
Db     180 ATGCTCAGGAGGCAGCTCGTCTGGTGGCACCTGCTGGCTTTGCTTTCCTCCCATTTTGC 239

Qy      21 LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40
           ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db     240 CTGTGTCAAGATGAATACATGGAGTCTCCACAAGCTGGAGGACTGCCCCCAGACTGCAGC 299

Qy      41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
           ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db     300 AAGTGTTGCCATGGAGATTATGGATTCCGTGGTTACCAAGGGCCCCCTGGACCCCCAGGT 359

Qy      61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     360 CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGAAATAACGGAGCCACTGGCCACGAA 419

Qy      81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     420 GGGGCCAAGGGTGAGAAAGGAGACAAAGGCGACCTGGGGCCTCGAGGGGAACGGGGGCAG 479

Qy     101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe 120
           ||||||||||||||   ||||||||||||||:::||||||||||||||||||||||||||
Db     480 CATGGCCCCAAAGGATAGAAGGGATACCCAGGGGTGCCACCAGAGCTGCAGATTGCGTTC 539

Qy     121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     540 ATGGCTTCTCTAGCGACTCACTTCAGCAATCAGAACAGTGGCATTATCTTCAGCAGTGTT 599

Qy     141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     600 GAGACCAACATTGGAAACTTCTTCGATGTCATGACTGGTAGATTTGGGGCCCCCGTATCA 659

Qy     161 GlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluValTyrVal 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     660 GGCGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGACGTGGAGGAAGTGTATGTG 719

Qy     181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200
           ||||||||||||||||||||||||||||||||||||||||||||||   ||||||||
Db     720 TACCTTATGCACAATGGTAACACGGTGTTCAGCATGTACAGCTATGAAACAAAGGGAAAA 779

Qy     201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTrpLeu 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     780 TCAGATACATCCAGCAACCATGCAGTGCTGAAGTTGGCCAAAGGAGATGAAGTCTGGCTA 839

Qy     221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     840 AGAATGGGCAACGGTGCCCTCCATGGGGACCACCAGCGCTTCTCTACCTTCGCAGGCTTT 899

Qy     241 LeuLeuPheGluThrLys 246
           ||||||||||||||||||
Db     900 CTGCTTTTTGAAACTAAG 917
```

```
RESULT 16
AAD12584
ID   AAD12584 standard; cDNA; 1927 BP.
XX
AC   AAD12584;
XX
DT   25-SEP-2001  (first entry)
XX
DE   Human protein having hydrophobic domain encoding cDNA clone HP10781.
XX
KW   Human; hydrophobic domain; gene therapy; nutritional supplement;
KW   cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial;
KW   multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
KW   haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic;
KW   Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;
KW   haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
KW   contraceptive; antiinfertility; antiinflammatory; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             89..760
FT                   /*tag= a
FT                   /product= "Human protein having hydrophobic domain"
FT                   /note= "CDS is specifically is claimed in claim 3"
FT   sig_peptide     89..157
FT                   /*tag= b
FT   mat_peptide     158..757
FT                   /*tag= c
FT                   /product= "Mature human protein with hydrophobic domain"
XX
PN   WO200149728-A2.
XX
PD   12-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-JP09359.
XX
PR   06-JAN-2000; 2000JP-0000585.
PR   06-JAN-2000; 2000JP-0000588.
PR   11-JAN-2000; 2000JP-0002299.
PR   03-FEB-2000; 2000JP-0026862.
PR   03-MAR-2000; 2000JP-0058367.
XX
PA   (PROT-) PROTEGENE INC.
PA   (SAGA ) SAGAMI CHEM RES CENT.
XX
PI   Kato S,  Kimura T;
XX
DR   WPI; 2001-418355/44.
DR   P-PSDB; AAE06589.
XX
PT   Human proteins with hydrophobic domains and the nucleic acids encoding
PT   them, useful for preventing diagnosing and treating e.g. cancer,
PT   Alzheimer's and inflammation -
XX
PS   Claim 4; Page 352-354; 563pp; English.
XX
CC   The present sequence is human protein with hydrophobic domain encoding
CC   cDNA clone HP10781. The polynucleotide and polypeptide of the invention
CC   may be used in the prevention, diagnosis and treatment of diseases
CC   associated with inappropriate polypeptide expression. The polynucleotides
CC   may be used to produce the polypeptide, by inserting the nucleic acids
CC   into a host cell and culturing the cell to express the protein. The
CC   polynucleotides and its complementary sequences may also be used as DNA
CC   probes in diagnostic assays and also used in gene therapy. The
CC   polypeptides may also be used as antigens in the production of antibodies
CC   and in assays to identify modulators of polypeptide expression and
CC   activity. The polypeptides and nucleic acids may be used as nutritional
CC   supplements, to modulate cytokine and cell proliferation activity, to
CC   modulate immune stimulation or suppression (e.g. for the treatment of
CC   microbial infections and autoimmune disorders such as multiple sclerosis,
CC   rheumatoid arthritis and insulin-dependent diabetes), to modulate
```

```
CC   haematopoiesis, to modulate tissue growth activity (e.g. for the
CC   treatment of Parkinson's disease, Huntington's disease and Alzheimer's
CC   disease), to modulate activin and inhibin activity (e.g. for controlling
CC   fertility), to modulate chemotactic and chemokinetic activity, to
CC   modulate haemostatic and thrombolytic activity, to modulate receptor
CC   ligand activity, to modulate inflammation and to inhibit tumour growth.
XX
SQ   Sequence 1927 BP; 550 A; 416 C; 452 G; 509 T; 0 other;

Alignment Scores:
Pred. No.:              2.22e-93        Length:         1927
Score:                  1291.50         Matches:        245
Percent Similarity:     76.80%          Conservative:   0
Best Local Similarity:  76.80%          Mismatches:     1
Query Match:            94.48%          Indels:         74
DB:                     22              Gaps:           1

US-10-036-041-2 (1-246) x AAD12584 (1-1927)

Qy       1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      89 ATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTCCTCCCTTTTTGC 148

Qy      21 LeuCysGlnAspGluTyrMetGlu---------------------------------- 28
           |||||||||||||||||||||||
Db     149 CTGTGTCAAGATGAATACATGGAGGTGAGCGGAAGAACTAATAAAGTGGTGGCAAGAATA 208

Qy      28 ---------------------------------------------------------- 28

Db     209 GTGCAAAGCCACCAGCAGACTGGCCGTAGCGGCTCCAGGAGGGAGAAAGTGAGAGAGCGG 268

Qy      28 ---------------------------------------------------------- 28

Db     269 AGCCATCCTAAAACTGGGACTGTGGATAATAACACTTCTACAGACCTAAAATCCCTGAGA 328

Qy      28 ---------------------------------------------------------- 28

Db     329 CCAGATGAGCTACCGCACCCCGAGGTAGATGACCTAGCCCAGATCACCACATTCTGGGGC 388

Qy      29 ---SerProGlnThrGlyGlyLeuProProAspCysSerLysCysCysHisGlyAspTyr 47
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     389 CAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTAC 448

Qy      48 SerPheArgGlyTyrGlnGlyProProGlyProProGlyProProGlyIleProGlyAsn 67
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     449 AGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAAC 508

Qy      68 HisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGluGlyAlaLysGlyGluLysGly 87
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     509 CATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGC 568

Qy      88 AspLysGlyAspLeuGlyProArgGlyGluArgGlyGlnHisGlyProLysGlyGluLys 107
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     569 GACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAG 628

Qy     108 GlyTyrProGlyIleProProGluLeuGlnIleAlaPheMetAlaSerLeuAlaThrHis 127
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     629 GGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCAC 688

Qy     128 PheSerAsnGlnAsnSerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhe 147
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     689 TTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTC 748

Qy     148 PheAspValMetThrGlyArgPheGlyAlaProValSerGlyValTyrPhePheThrPhe 167
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     749 TT-GATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGGTGTGTATTTCTTCACCTTC 807

Qy     168 SerMetMetLysHisGluAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsn 187
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     808 AGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATGGCAAC 867

Qy     188 ThrValPheSerMetTyrSerTyrGluMetLysGlyLysSerAspThrSerSerAsnHis 207
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     868 ACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCAATCAT 927

Qy     208 AlaValLeuLysLeuAlaLysGlyAspGluValTrpLeuArgMetGlyAsnGlyAlaLeu 227
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     928 GCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTC 987

Qy     228 HisGlyAspHisGlnArgPheSerThrPheAlaGlyPheLeuLeuPheGluThrLys 246
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     988 CATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTAAG 1044

RESULT 17
AAF94076
ID   AAF94076 standard; DNA; 810 BP.
XX
AC   AAF94076;
XX
DT   23-MAY-2001  (first entry)
XX
DE   Primer specific for DNA encoding secretory/membrane protein SEQ ID 510.
XX
KW   Human; secretory protein; membrane protein; vaccine; gene therapy;
KW   rheumatoid arthritis; diabetes; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   EP1067182-A2.
XX
PD   10-JAN-2001.
XX
PF   07-JUL-2000; 2000EP-0114090.
XX
PR   08-JUL-1999;   99JP-0194179.
PR   11-JAN-2000; 2000JP-0118775.
PR   02-MAY-2000; 2000JP-0183766.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Kawai Y,  Sugiyama T,  Hayashi K;
XX
DR   WPI; 2001-093989/11.
XX
PT   Nucleic acids encoding secretory proteins/membrane proteins, useful in
PT   gene therapy or as candidate target molecules in drug development -
XX
PS   Claim 4; SEQ ID 510; 609pp + CD ROM; English.
XX
CC   This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC   which encode human secretory or membrane proteins represented by
CC   AAB88317 - AAB88419. Included in the invention are primers
CC   AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
CC   cDNA sequences of the invention. The invention also includes methods for
CC   the production of antibodies directed against the proteins, and cDNA
CC   sequences, which can be used in vaccines. The polynucleotide sequences
CC   can be used in gene therapy. The polynucleotide sequences and the
CC   proteins they encode may be used in the prevention, treatment and
CC   diagnosis of diseases associated with inappropriate secretory
CC   protein/membrane protein expression. The nucleic acids and complementary
CC   sequences may also be used as DNA probes in diagnostic assays
CC   (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
CC   presence of similar nucleic acid sequences in samples. They may also be
CC   used to study the expression and function of secretory proteins/membrane
CC   polypeptides and their role in metabolism. The polypeptides may be used
CC   as antigens in the production of antibodies against them and in assays to
CC   identify modulators (agonists and antagonists) of expression and
CC   activity. The antibodies and antagonists may also be used as therapeutic
CC   agents to down regulate expression and activity. The antibodies may also
CC   be used as diagnostic agents for detecting the presence of the
CC   polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC   (ELISA). Examples of diseases which may be treated include rheumatoid
CC   arthritis and diabetes.
XX
SQ   Sequence 810 BP; 200 A; 201 C; 218 G; 188 T; 3 other;
```

```
Alignment Scores:
Pred. No.:                3.1e-91       Length:          810
Score:                    1259.00       Matches:         234
Percent Similarity:       97.51%        Conservative:    1
Best Local Similarity:    97.10%        Mismatches:      6
Query Match:              92.10%        Indels:          2
DB:                       22            Gaps:            0

US-10-036-041-2 (1-246) x AAF94076 (1-810)

Qy       1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      89 ATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTCCTCCCTTTTTGC 148

Qy      21 LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     149 CTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGT 208

Qy      41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     209 AAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGC 268

Qy      61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     269 CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAA 328

Qy      81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     329 GGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAG 388

Qy     101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     389 CATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTC 448

Qy     121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     449 ATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTT 508

Qy     141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     509 GAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCA 568

Qy     161 GlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluValTyrVal 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     569 GGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTG 628

Qy     181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200
           ||||||||||||||||||||||||||||||:::||||||||||||||||||||||||||||
Db     629 TACCTTATGCACAATGGCAACACAGTCTTCAACATGTACAGCTATGAAATGAAGGGCAAA 688

Qy     201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTrpLeu 220
           |||||||||||||||||||||||||||||   |||||||||   ||||||||||||||||
Db     689 TCAGATACATCCAGCAATCATGCTGTGCTGAA-CTAGCCAAAANGGGATGAGGTTTGGCTG 747

Qy     221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
           ||||||||||||   ||||||||||||||||||||   ||||||||||||||||||||||
Db     748 CNAAT-GGCAATGGCGCTNTTCATGGGGACCACCAACGCTTCTTCACCTTTGCAGGATTC 806

Qy     241 Leu 241
           |||
Db     807 CTG 809

RESULT 18
AAI59230
ID   AAI59230 standard; cDNA; 1792 BP.
XX
AC   AAI59230;
XX
DT   22-OCT-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 1433.
XX
KW   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia; ss.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US34263.
XX
PR   21-JAN-2000; 2000US-0488725.
PR   25-APR-2000; 2000US-0552317.
PR   09-JUL-2000; 2000US-0598042.
PR   19-JUL-2000; 2000US-0620312.
PR   03-AUG-2000; 2000US-0653450.
PR   14-SEP-2000; 2000US-0662191.
PR   19-OCT-2000; 2000US-0693036.
PR   29-NOV-2000; 2000US-0727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Asundi V,  Chen R,  Ma Y,  Qian XB,  Ren F,  Wang D;
PI   Wang J,  Wang Z,  Wehrman T,  Xu C,  Xue AJ,  Yang Y,  Zhang J;
PI   Zhao QA,  Zhou P,  Goodrich R,  Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   P-PSDB; AAM40074.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders
PT   such as central nervous system injuries -
XX
PS   Claim 1; SEQ ID NO 1433; 10078pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC   the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: Immune system suppression,
CC   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification.
XX
SQ   Sequence 1792 BP; 541 A; 352 C; 393 G; 506 T; 0 other;

Alignment Scores:
Pred. No.:                5.02e-87      Length:          1792
Score:                    1211.00       Matches:         219
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              88.59%        Indels:          0
DB:                       22            Gaps:            0

US-10-036-041-2 (1-246) x AAI59230 (1-1792)

Qy      28 GluSerProGlnThrGlyGlyLeuProProAspCysSerLysCysCysHisGlyAspTyr 47
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTAC 300

Qy      48 SerPheArgGlyTyrGlnGlyProProGlyProProGlyProProGlyIleProGlyAsn 67
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAAC 360
```

```
Qy      68 HisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGluGlyAlaLysGlyGluLysGly 87
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGC 420

Qy      88 AspLysGlyAspLeuGlyProArgGlyGluArgGlyGlnHisGlyProLysGlyGluLys 107
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAG 480

Qy     108 GlyTyrProGlyIleProProGluLeuGlnIleAlaPheMetAlaSerLeuAlaThrHis 127
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCAC 540

Qy     128 PheSerAsnGlnAsnSerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhe 147
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 TTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTC 600

Qy     148 PheAspValMetThrGlyArgPheGlyAlaProValSerGlyValTyrPhePheThrPhe 167
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGGTGTGTATTTCTTCACCTTC 660

Qy     168 SerMetMetLysHisGluAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsn 187
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 AGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATGGCAAC 720

Qy     188 ThrValPheSerMetTyrSerTyrGluMetLysGlyLysSerAspThrSerSerAsnHis 207
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 ACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCAATCAT 780

Qy     208 AlaValLeuLysLeuAlaLysGlyAspGluValTrpLeuArgMetGlyAsnGlyAlaLeu 227
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 GCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTC 840

Qy     228 HisGlyAspHisGlnArgPheSerThrPheAlaGlyPheLeuLeuPheGluThrLys 246
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTAAG 897
```

RESULT 19
AAI99523
ID  AAI99523 standard; cDNA; 1620 BP.
XX
AC  AAI99523;
XX
DT  07-JAN-2002  (first entry)
XX
DE  Human polynucleotide SEQ ID NO 21.
XX
KW  Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW  antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW  vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW  cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW  neurological disease; infection; human; secreted protein; ss.
XX
OS  Homo sapiens.
XX
PN  WO200155173-A2.
XX
PD  02-AUG-2001.
XX
PF  17-JAN-2001; 2001WO-US01356.
XX
PR  31-JAN-2000; 2000US-0179065.
PR  04-FEB-2000; 2000US-0180628.
PR  24-FEB-2000; 2000US-0184664.
PR  02-MAR-2000; 2000US-0186350.
PR  16-MAR-2000; 2000US-0189874.
PR  17-MAR-2000; 2000US-0190076.
PR  18-APR-2000; 2000US-0198123.
PR  19-MAY-2000; 2000US-0205515.
PR  07-JUN-2000; 2000US-0209467.
PR  28-JUN-2000; 2000US-0214886.
PR  30-JUN-2000; 2000US-0215135.
PR  07-JUL-2000; 2000US-0216647.
PR  07-JUL-2000; 2000US-0216880.
PR  11-JUL-2000; 2000US-0217487.
PR  11-JUL-2000; 2000US-0217496.
PR  14-JUL-2000; 2000US-0218290.
PR  26-JUL-2000; 2000US-0220963.
PR  26-JUL-2000; 2000US-0220964.
PR  14-AUG-2000; 2000US-0224518.
PR  14-AUG-2000; 2000US-0224519.
PR  14-AUG-2000; 2000US-0225213.
PR  14-AUG-2000; 2000US-0225214.
PR  14-AUG-2000; 2000US-0225266.
PR  14-AUG-2000; 2000US-0225267.
PR  14-AUG-2000; 2000US-0225268.
PR  14-AUG-2000; 2000US-0225270.
PR  14-AUG-2000; 2000US-0225447.
PR  14-AUG-2000; 2000US-0225757.
PR  14-AUG-2000; 2000US-0225758.
PR  14-AUG-2000; 2000US-0225759.
PR  18-AUG-2000; 2000US-0226279.
PR  22-AUG-2000; 2000US-0226681.
PR  22-AUG-2000; 2000US-0226868.
PR  22-AUG-2000; 2000US-0227182.
PR  23-AUG-2000; 2000US-0227009.
PR  30-AUG-2000; 2000US-0228924.
PR  01-SEP-2000; 2000US-0229287.
PR  01-SEP-2000; 2000US-0229343.
PR  01-SEP-2000; 2000US-0229344.
PR  01-SEP-2000; 2000US-0229345.
PR  05-SEP-2000; 2000US-0229509.
PR  05-SEP-2000; 2000US-0229513.
PR  06-SEP-2000; 2000US-0230437.
PR  06-SEP-2000; 2000US-0230438.
PR  08-SEP-2000; 2000US-0231242.
PR  08-SEP-2000; 2000US-0231243.
PR  08-SEP-2000; 2000US-0231244.
PR  08-SEP-2000; 2000US-0231413.
PR  08-SEP-2000; 2000US-0231414.
PR  08-SEP-2000; 2000US-0232080.
PR  08-SEP-2000; 2000US-0232081.
PR  12-SEP-2000; 2000US-0231968.
PR  14-SEP-2000; 2000US-0232397.
PR  14-SEP-2000; 2000US-0232398.
PR  14-SEP-2000; 2000US-0232399.
PR  14-SEP-2000; 2000US-0232400.
PR  14-SEP-2000; 2000US-0232401.
PR  14-SEP-2000; 2000US-0233063.
PR  14-SEP-2000; 2000US-0233064.
PR  14-SEP-2000; 2000US-0233065.
PR  21-SEP-2000; 2000US-0234223.
PR  21-SEP-2000; 2000US-0234274.
PR  25-SEP-2000; 2000US-0234997.
PR  25-SEP-2000; 2000US-0234998.
PR  26-SEP-2000; 2000US-0235484.
PR  27-SEP-2000; 2000US-0235834.
PR  27-SEP-2000; 2000US-0235836.
PR  29-SEP-2000; 2000US-0236327.
PR  29-SEP-2000; 2000US-0236367.
PR  29-SEP-2000; 2000US-0236368.
PR  29-SEP-2000; 2000US-0236369.
PR  29-SEP-2000; 2000US-0236370.
PR  02-OCT-2000; 2000US-0236802.
PR  02-OCT-2000; 2000US-0237037.
PR  02-OCT-2000; 2000US-0237038.
PR  02-OCT-2000; 2000US-0237039.
PR  02-OCT-2000; 2000US-0237040.
PR  13-OCT-2000; 2000US-0239935.
PR  13-OCT-2000; 2000US-0239937.
PR  20-OCT-2000; 2000US-0240960.
PR  20-OCT-2000; 2000US-0241221.
PR  20-OCT-2000; 2000US-0241785.
PR  20-OCT-2000; 2000US-0241786.
PR  20-OCT-2000; 2000US-0241787.
PR  20-OCT-2000; 2000US-0241808.

```
PR   20-OCT-2000; 2000US-0241809.
PR   20-OCT-2000; 2000US-0241826.
PR   01-NOV-2000; 2000US-0244617.
PR   08-NOV-2000; 2000US-0246474.
PR   08-NOV-2000; 2000US-0246475.
PR   08-NOV-2000; 2000US-0246476.
PR   08-NOV-2000; 2000US-0246477.
PR   08-NOV-2000; 2000US-0246478.
PR   08-NOV-2000; 2000US-0246523.
PR   08-NOV-2000; 2000US-0246524.
PR   08-NOV-2000; 2000US-0246525.
PR   08-NOV-2000; 2000US-0246526.
PR   08-NOV-2000; 2000US-0246527.
PR   08-NOV-2000; 2000US-0246528.
PR   08-NOV-2000; 2000US-0246532.
PR   08-NOV-2000; 2000US-0246609.
PR   08-NOV-2000; 2000US-0246610.
PR   08-NOV-2000; 2000US-0246611.
PR   08-NOV-2000; 2000US-0246613.
PR   17-NOV-2000; 2000US-0249207.
PR   17-NOV-2000; 2000US-0249208.
PR   17-NOV-2000; 2000US-0249209.
PR   17-NOV-2000; 2000US-0249210.
PR   17-NOV-2000; 2000US-0249211.
PR   17-NOV-2000; 2000US-0249212.
PR   17-NOV-2000; 2000US-0249213.
PR   17-NOV-2000; 2000US-0249214.
PR   17-NOV-2000; 2000US-0249215.
PR   17-NOV-2000; 2000US-0249216.
PR   17-NOV-2000; 2000US-0249217.
PR   17-NOV-2000; 2000US-0249218.
PR   17-NOV-2000; 2000US-0249244.
PR   17-NOV-2000; 2000US-0249245.
PR   17-NOV-2000; 2000US-0249264.
PR   17-NOV-2000; 2000US-0249265.
PR   17-NOV-2000; 2000US-0249297.
PR   17-NOV-2000; 2000US-0249299.
PR   17-NOV-2000; 2000US-0249300.
PR   01-DEC-2000; 2000US-0250160.
PR   01-DEC-2000; 2000US-0250391.
PR   05-DEC-2000; 2000US-0251030.
PR   05-DEC-2000; 2000US-0251988.
PR   05-DEC-2000; 2000US-0256719.
PR   06-DEC-2000; 2000US-0251479.
PR   08-DEC-2000; 2000US-0251856.
PR   08-DEC-2000; 2000US-0251868.
PR   08-DEC-2000; 2000US-0251869.
PR   08-DEC-2000; 2000US-0251989.
PR   08-DEC-2000; 2000US-0251990.
PR   11-DEC-2000; 2000US-0254097.
PR   05-JAN-2001; 2001US-0259678.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
DR   WPI; 2001-451924/48.
DR   P-PSDB; AAM99925.
XX
PT   New nucleic acids and polypeptides, useful for treating, preventing or
PT   ameliorating human disorders and diseases -
XX
PS   Claim 1; SEQ ID NO 21; 465pp + Sequence Listing; English.
XX
CC   The invention relates to novel human polynucleotides (AAI99513-AAI99538)
CC   and the encoded proteins (AAM99915-AAM99934) which are useful for
CC   preventing, treating or ameliorating medical conditions e.g. by protein
CC   or gene therapy. The genes are isolated from a range of human tissues
CC   disclosed in the specification. The nucleic acids, proteins, antibodies
CC   and (ant)agonists are useful in the diagnosis, treatment and prevention
CC   of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the
CC   adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
CC   lung, or urogenital; (b) immune disorders e.g. Addison's disease,
CC   allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
CC   diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
CC   arthritis and ulcerative colitis; (c) cardiovascular disorders such as
CC   myocardial ischaemias; (d) wound healing; (e) neurological diseases
CC   e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as
CC   viral, bacterial, fungal and parasitic infections.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1620 BP; 485 A; 332 C; 360 G; 440 T; 3 other;

Alignment Scores:
Pred. No.:                7.73e-87        Length:          1620
Score:                    1208.00         Matches:         218
Percent Similarity:       100.00%         Conservative:    1
Best Local Similarity:    99.54%          Mismatches:      0
Query Match:              88.37%          Indels:          0
DB:                       22              Gaps:            0

US-10-036-041-2 (1-246) x AAI99523 (1-1620)

Qy      28 GluSerProGlnThrGlyGlyLeuProProAspCysSerLysCysCysHisGlyAspTyr 47
           :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      21 CAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTAC 80

Qy      48 SerPheArgGlyTyrGlnGlyProProGlyProProGlyProProGlyIleProGlyAsn 67
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      81 AGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAAC 140

Qy      68 HisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGluGlyAlaLysGlyGluLysGly 87
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     141 CATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGC 200

Qy      88 AspLysGlyAspLeuGlyProArgGlyGluArgGlyGlnHisGlyProLysGlyGluLys 107
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     201 GACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAG 260

Qy     108 GlyTyrProGlyIleProProGluLeuGlnIleAlaPheMetAlaSerLeuAlaThrHis 127
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     261 GGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCAC 320

Qy     128 PheSerAsnGlnAsnSerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhe 147
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     321 TTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTC 380

Qy     148 PheAspValMetThrGlyArgPheGlyAlaProValSerGlyValTyrPhePheThrPhe 167
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     381 TTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGGTGTGTATTTCTTCACCTTC 440

Qy     168 SerMetMetLysHisGluAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsn 187
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     441 AGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATGGCAAC 500

Qy     188 ThrValPheSerMetTyrSerTyrGluMetLysGlyLysSerAspThrSerSerAsnHis 207
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     501 ACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCAATCAT 560

Qy     208 AlaValLeuLysLeuAlaLysGlyAspGluValTrpLeuArgMetGlyAsnGlyAlaLeu 227
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     561 GCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTC 620

Qy     228 HisGlyAspHisGlnArgPheSerThrPheAlaGlyPheLeuLeuPheGluThrLys 246
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     621 CATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTAAG 677

RESULT 20
AAC64063
ID   AAC64063 standard; DNA; 738 BP.
XX
AC   AAC64063;
XX
DT   19-FEB-2001  (first entry)
```

XX
DE Human zacrp3 degenerate DNA, SEQ ID NO:10.
XX
KW Human zacrp3; adipocyte complement related protein homologue;
KW ACRP30; C1q domain; collagen-like domain; energy balance modulation;
KW cellular metabolism; metabolic disorder; obesity; anorexia;
KW antimicrobial agent; infection; platelet aggregation inhibition;
KW adhesion; activation; vascular injury; antibacterial; antiviral; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200063377-A1.
XX
PD 26-OCT-2000.
XX
PF 19-APR-2000; 2000WO-US10454.
XX
PR 20-APR-1999; 99US-0294943.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Piddington CS, Bishop PD;
XX
DR WPI; 2000-665243/64.
XX
PT Novel zacrp3 polypeptides used to treat or prevent bacterial or viral
PT infections, for wound healing, improving blood flow, and to analyze
PT energy efficiency in mammals
XX
PS Claim 10; Page 115; 123pp; English.
XX
CC The invention relates to the human zacrp3 protein (AAB29580) and to
CC nucleic acids which encode it (AAC64058, AAC64063). Zacrp3 is a homogue
CC of adipocyte complement related protein (ACRP30) and contains a
CC collagen-like domain comprising Gly-Xaa-Xaa or Gly-Xaa-Pro repeats, and a
CC C-terminal C1q domain comprising 10 beta-strands. The zacrp3 gene is
CC located on chromosome 5p12. The invention also relates to zacrp3
CC fragments, fusion proteins containing zacrp3 polypeptides,
CC zacrp3-specific antibodies, expression constructs and host cells
CC comprising zacrp3 nucleic acids, and methods of recombinant production of
CC zacrp3. Human zacrp3, and its agonists and antagonists may be used in the
CC study and modulation of cellular metabolism and energy balance in
CC mammals, and may therefore be used to treat disorders such as obesity and
CC anorexia, and conditions associated with these disorders. Due to its C1q
CC like domain, zacrp3 and zacrp3-containing fusion proteins may be useful
CC as antimicrobial agents, promoting lysis or phagocytosis of infectious
CC organisms such as bacteria or viruses. Zacrp3, its fragments, fusion
CC proteins, antibodies and activity modulators may also be used to inhibit
CC collagen-induced platelet aggregation, adhesion, or activation, and may
CC therefore have potential for promoting blood flow within the vasculature
CC of a mammal e.g., to treat injury to the vasculature or other collagenous
CC tissue. Human zacrp3 and its antibodies may additionally be used to study
CC dimerisation and oligomerisation. The present sequence represents a
CC degenerate DNA sequence encoding human zacrp3.
XX
SQ Sequence 738 BP; 130 A; 74 C; 145 G; 99 T; 290 other;

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 2.7e-84 | Length: | 738 |
| Score: | 1171.00 | Matches: | 205 |
| Percent Similarity: | 83.33% | Conservative: | 0 |
| Best Local Similarity: | 83.33% | Mismatches: | 41 |
| Query Match: | 85.66% | Indels: | 0 |
| DB: | 21 | Gaps: | 0 |

US-10-036-041-2 (1-246) x AAC64063 (1-738)

```
Qy       1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys 20
           |||  |||  |||  ||||||||||||     |||  ||||||  |||||||||
Db       1 ATGYTNTGGMGNCARYTNATHTAYTGGCARYTNYTNGCNYTNTTYTTYYTNCCNTTYTGY 60

Qy      21 LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40
                ||||||||||||||||||||  ||||||||||||||  |||||||||||||
Db      61 YTNTGYCARGAYGARTAYATGGARWSNCCNCARACNGGNGGNYTNCCNCCNGAYTGYWSN 120

Qy      41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
           ||||||||||||||||||||  |||  ||||||||||||||||||||||||||||||
Db     121 AARTGYTGYCAYGGNGAYTAYWSNTTYMGNGGNTAYCARGGNCCNCCNGGNCCNCCNGGN 180

Qy      61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CCNCCNGGNATHCCNGGNAAYCAYGGNAAYAAYGGNAAYAAYGGNGCNACNGGNCAYGAR 240

Qy      81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100
           ||||||||||||||||||||||||||||||||  ||||||  ||||||  ||||||
Db     241 GGNGCNAARGGNGARAARGGNGAYAARGGNGAYYTNGGNCCNMGNGGNGARMGNGGNCAR 300

Qy     101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe 120
           ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db     301 CAYGGNCCNAARGGNGARAARGGNTAYCCNGGNATHCCNCCNGARYTNCARATHGCNTTY 360

Qy     121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
           ||||||  ||||||||||  ||||||||  ||||||||||  |||
Db     361 ATGGCNWSNYTNGCNACNCAYTTYWSNAAYCARAAYWSNGGNATHATHTTYWSNWSNGTN 420

Qy     141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
           ||||||||||||||||||||||||||||||||||||  ||||||||||||||
Db     421 GARACNAAYATHGGNAAYTTYTTYGAYGTNATGACNGGNMGNTTYGGNGCNCCNGTNWSN 480

Qy     161 GlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluValTyrVal 180
           ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db     481 GGNGTNTAYTTYTTYACNTTYWSNATGATGAARCAYGARGAYGTNGARGARGTNTAYGTN 540

Qy     181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200
           |||  ||||||||||||||||||||||  ||||||  ||||||||||||||||||
Db     541 TAYYTNATGCAYAAYGGNAAYACNGTNTTYWSNATGTAYWSNTAYGARATGAARGGNAAR 600

Qy     201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTrpLeu 220
           ||||||  ||||||||||||  |||  ||||||||||||||||||||
Db     601 WSNGAYACNWSNWSNAAYCAYGCNGTNYTNAARYTNGCNAARGGNGAYGARGTNTGGYTN 660

Qy     221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
           ||||||||||||||  ||||||||||||||  |||  ||||||||||||||
Db     661 MGNATGGGNAAYGGNGCNYTNCAYGGNGAYCAYCARMGNTTYWSNACNTTYGCNGGNTTY 720

Qy     241 LeuLeuPheGluThrLys 246
           ||||||||||||||||||
Db     721 YTNYTNTTYGARACNAAR 738
```

RESULT 21
AAI61016/c
ID AAI61016 standard; cDNA; 1799 BP.
XX
AC AAI61016;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 5005.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.

```
PR   25-APR-2000; 2000US-0552317.
PR   09-JUL-2000; 2000US-0598042.
PR   19-JUL-2000; 2000US-0620312.
PR   03-AUG-2000; 2000US-0653450.
PR   14-SEP-2000; 2000US-0662191.
PR   19-OCT-2000; 2000US-0693036.
PR   29-NOV-2000; 2000US-0727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI   Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI   Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   P-PSDB; AAM41860.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders
PT   such as central nervous system injuries -
XX
PS   Claim 1; SEQ ID NO 5005; 10078pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC   the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: Immune system suppression,
CC   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification.
XX
SQ   Sequence 1799 BP; 531 A; 389 C; 344 G; 535 T; 0 other;

Alignment Scores:
Pred. No.:                4.88e-59        Length:         1799
Score:                    858.50          Matches:        169
Percent Similarity:       83.66%          Conservative:   0
Best Local Similarity:    83.66%          Mismatches:     1
Query Match:              62.80%          Indels:         33
DB:                       22              Gaps:           1

US-10-036-041-2 (1-246) x AAI61016 (1-1799)

Qy      77 ThrGlyHisGluGlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGly 96
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1797 ACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGG 1738

Qy      97 GluArgGlyGlnHisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeu 116
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1737 GAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACT- 1679

Qy     116 ------------------------------------------------------------ 116

Db    1678 TCAGGCTGGAGTGCAGTGGTGTGATCTTGGCTCACTGCAGCCTCCACCAAGGTTCAAGCG 1619

Qy     117 ----------------------------------GlnIleAlaPheMetAlaSerLeu 124
                                               |||||||||||||||||||||||
Db    1618 ATTCTCTTGCCTCAACCTCTGGAGTAGCTGGGATTACAGATTGCATTCATGGCTTCTCTG 1559

Qy     125 AlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerValGluThrAsnIle 144
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1558 GCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATT 1499

Qy     145 GlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSerGlyValTyrPhe 164
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    1498 GGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGGTGTGTATTTC 1439

Qy     165 PheThrPheSerMetMetLysHisGluAspValGluGluValTyrValTyrLeuMetHis 184
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1438 TTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCAC 1379

Qy     185 AsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLysSerAspThrSer 204
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1378 AATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCC 1319

Qy     205 SerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTrpLeuArgMetGlyAsn 224
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1318 AGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAAT 1259

Qy     225 GlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPheLeuLeuPheGlu 244
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1258 GGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAA 1199

Qy     245 ThrLys 246
           ||||||
Db    1198 ACTAAG 1193

RESULT 22
ABK35221
ID   ABK35221 standard; cDNA; 1608 BP.
XX
AC   ABK35221;
XX
DT   08-MAY-2002  (first entry)
XX
DE   Human cDNA encoding secreted protein #359.
XX
KW   Human; secreted protein; gene; ss; nutritional supplement; haemophilia;
KW   viral infection; bacterial infection; fungal infection; diabetes; asthma;
KW   autoimmune disorder; rheumatoid arthritis; multiple sclerosis; tumour;
KW   autoimmune thyroiditis; allergic reaction; neurodegenerative disease;
KW   Alzheimer's disease; Parkinson's disease; liver fibrosis; cancer; ulcer;
KW   coagulation disorder; inflammatory disorder; Crohn's disease; incision;
KW   tissue regeneration; wound healing; burn; haematopoiesis;
KW   myeloid cell deficiency; lymphoid cell deficiency.
XX
OS   Homo sapiens.
XX
PN   WO200177288-A2.
XX
PD   18-OCT-2001.
XX
PF   29-MAR-2001; 2001WO-US10224.
XX
PR   06-APR-2000; 2000US-195582P.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Wong GG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;
PI   Gulukota K, Graham JR;
XX
DR   WPI; 2002-179321/23.
XX
PT   Five hundred and ninety two polynucleotides derived from a variety of
PT   human tissue sources which encode secreted proteins, useful for
PT   treating immune deficiencies and disorders such as autoimmune disorders
PT   -
XX
PS   Claim 1; Page 261-262; 372pp; English.
XX
CC   The invention relates to 592 polynucleotides which have been derived from
CC   a variety of human tissue sources and which encode novel secreted
CC   proteins. The polynucleotides can be used as probes for the
CC   identification and isolation of full length cDNA and genomic DNA. The
CC   polynucleotides and proteins can also be used as nutritional supplements.
CC   The proteins are useful in the treatment of various immune deficiencies
CC   and disorders such as viral infections, bacterial infections, fungal
CC   infections, autoimmune disorders (e.g. rheumatoid arthritis, multiple
```

```
CC   sclerosis, autoimmune thyroiditis and diabetes) and allergic reactions
CC   and conditions (e.g. asthma). They are also useful for treating
CC   neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's
CC   disease), liver fibrosis, coagulation disorders (e.g. haemophilia),
CC   inflammatory disorders (e.g. Crohn's disease) and tumours. They are also
CC   useful for tissue regeneration, for wound healing and in the treatment of
CC   burns, incisions and ulcers. The proteins are also useful for regulating
CC   haematopoiesis and for treating myeloid or lymphoid cell deficiencies.
CC   Sequences ABK34863-ABK35454 represent polynucleotides of the invention.
XX
SQ   Sequence 1608 BP; 487 A; 305 C; 339 G; 477 T; 0 other;

Alignment Scores:
Pred. No.:                2.43e-58      Length:          1608
Score:                    849.00        Matches:         159
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              62.11%        Indels:          0
DB:                       24            Gaps:            0

US-10-036-041-2 (1-246) x ABK35221 (1-1608)

Qy      88 AspLysGlyAspLeuGlyProArgGlyGluArgGlyGlnHisGlyProLysGlyGluLys 107
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 GACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAG 61

Qy     108 GlyTyrProGlyIleProProGluLeuGlnIleAlaPheMetAlaSerLeuAlaThrHis 127
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 GGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCAC 121

Qy     128 PheSerAsnGlnAsnSerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhe 147
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     122 TTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTC 181

Qy     148 PheAspValMetThrGlyArgPheGlyAlaProValSerGlyValTyrPhePheThrPhe 167
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     182 TTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGGTGTGTATTTCTTCACCTTC 241

Qy     168 SerMetMetLysHisGluAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsn 187
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     242 AGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATGGCAAC 301

Qy     188 ThrValPheSerMetTyrSerTyrGluMetLysGlyLysSerAspThrSerSerAsnHis 207
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     302 ACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCAATCAT 361

Qy     208 AlaValLeuLysLeuAlaLysGlyAspGluValTrpLeuArgMetGlyAsnGlyAlaLeu 227
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     362 GCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTC 421

Qy     228 HisGlyAspHisGlnArgPheSerThrPheAlaGlyPheLeuLeuPheGluThrLys 246
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     422 CATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTAAG 478

RESULT 23
AAC02874
ID   AAC02874 standard; cDNA; 471 BP.
XX
AC   AAC02874;
XX
DT   06-OCT-2000  (first entry)
XX
DE   Human secreted protein 5' EST, SEQ ID NO: 2872.
XX
KW   Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW   gene therapy; chromosome mapping; ss.
XX
OS   Homo sapiens.
XX
PN   EP1033401-A2.
XX
PD   06-SEP-2000.
XX
PF   21-FEB-2000; 2000EP-0200610.
XX
PR   26-FEB-1999;   99US-0122487.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J,  Duclert A,  Giordano J;
XX
DR   WPI; 2000-500381/45.
DR   P-PSDB; AAG02868.
XX
PT   New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT   obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT   diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS   Claim 1; SEQ ID 2872; 71pp + CD-ROM; English.
XX
CC   The present sequence is one of a large number of 5' ESTs derived from
CC   mRNAs encoding secreted proteins. An ORF has been identified within the
CC   sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
CC   derived from 30 different tissues. EST sequences usually correspond
CC   mainly to the 3' untranslated region (UTR) of the mRNA because they are
CC   often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
CC   well suited for isolating cDNA sequences derived from the 5' ends of
CC   mRNAs and even in those cases where longer cDNA sequences have been
CC   obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
CC   mRNAs with intact 5' ends and can therefore be used to obtain full length
CC   cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
CC   gene therapy and chromosome mapping procedures. They are used to obtain
CC   upstream regulatory sequences and to design expression and secretion
CC   vectors.
XX
SQ   Sequence 471 BP; 107 A; 130 C; 134 G; 99 T; 1 other;

Alignment Scores:
Pred. No.:                8.56e-49      Length:          471
Score:                    721.00        Matches:         127
Percent Similarity:       99.22%        Conservative:    0
Best Local Similarity:    99.22%        Mismatches:      1
Query Match:              52.74%        Indels:          1
DB:                       21            Gaps:            0

US-10-036-041-2 (1-246) x AAC02874 (1-471)

Qy       1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      88 ATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTCCTCCCTTTTTGC 147

Qy      21 LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     148 CTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGT 207

Qy      41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     208 AAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGC 267

Qy      61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     268 CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAA 327

Qy      81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     328 GGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAG 387

Qy     101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     388 CATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTC 447

Qy     121 MetAlaSerLeuAlaThrHisPhe 128
           |||||||||||   |||||||||
Db     448 ATGGCTTCTCTGGM-ACCCACTTC 470

RESULT 24
```

```
AAX39551
ID   AAX39551 standard; DNA; 472 BP.
XX
AC   AAX39551;
XX
DT   21-JUN-1999  (first entry)
XX
DE   Human secreted protein 5' EST SEQ ID No 149.
XX
KW   Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW   forensic; gene therapy; chromosome mapping; signal peptide;
KW   upstream regulatory sequence; cytokine activity; cell proliferation;
KW   differentiation; haematopoiesis regulation; tissue growth regulation;
KW   reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW   thrombolytic; anti-inflammatory; tumour inhibition; ds.
XX
OS   Homo sapiens.
XX
PN   WO9906551-A2.
XX
PD   11-FEB-1999.
XX
PF   31-JUL-1998;   98WO-IB01235.
XX
PR   01-AUG-1997;   97US-0905133.
XX
PA   (GEST ) GENSET.
XX
PI   Duclert A,  Dumas Milne Edwards J,  Lacroix B;
XX
DR   WPI; 1999-153781/13.
DR   P-PSDB; AAY11485.
XX
PT   New nucleic acids encoding human secreted - proteins obtained from
PT   cDNA libraries prepared from substantia nigra, cerebellum, surrenals
PT   and fetal brain tissue
XX
PS   Claim 1; Page 263; 434pp; English.
XX
CC   AAX39440 to AAX39597 represent 5' expressed sequence tags (ESTs) for
CC   human secreted proteins, and encode the proteins given in AAY11374 to
CC   AAY11531, respectively. The proteins given represent the signal peptide
CC   and an N-terminal fragment of a secreted protein. The nucleic acid
CC   sequences can be used for producing secreted human gene products. They
CC   can also be used to develop products for diagnosis and therapy. The
CC   proteins obtained may have cytokine activity, cell
CC   proliferation/differentiation activity, haematopoiesis regulating
CC   activity, tissue growth regulating activity, reproductive hormone
CC   regulating activity, chemotactic/ chemokinetic activity, haemostatic and
CC   thrombolytic activity, receptor/ ligand activity, anti-inflammatory
CC   activity, tumour inhibition activity or other activities. The products
CC   can be used in forensic, gene therapy and chromosome mapping procedures.
CC   The sequences can also be used for obtaining corresponding promoter
CC   sequences. The nucleic acids encoding the signal peptide can be used for
CC   directing extracellular secretion of a polypeptide or the insertion of a
CC   polypeptide into a membrane, or importing a polypeptide into a cell.
XX
SQ   Sequence 472 BP; 108 A; 130 C; 134 G; 99 T; 1 other;

Alignment Scores:
Pred. No.:              8.58e-49      Length:          472
Score:                  721.00        Matches:         127
Percent Similarity:     99.22%        Conservative:    0
Best Local Similarity:  99.22%        Mismatches:      1
Query Match:            52.74%        Indels:          1
DB:                     20            Gaps:            0

US-10-036-041-2 (1-246) x AAX39551 (1-472)

Qy       1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      89 ATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTCCTCCCTTTTTGC 148

Qy      21 LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     149 CTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGT 208

Qy      41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     209 AAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGC 268

Qy      61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     269 CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAA 328

Qy      81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     329 GGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAG 388

Qy     101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProGlyGluLeuGlnIleAlaPhe 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     389 CATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTC 448

Qy     121 MetAlaSerLeuAlaThrHisPhe 128
           ||||||||||||   |||||||||
Db     449 ATGGCTTCTCTGGM-ACCCACTTC 471

RESULT 25
AAF93419
ID   AAF93419 standard; cDNA; 546 BP.
XX
AC   AAF93419;
XX
DT   21-MAY-2001  (first entry)
XX
DE   cDNA encoding SRT protein isolated from prostate tissue SEQ ID 240.
XX
KW   Human; SRT; gene therapy; gene mapping; tissue typing; ss.
XX
OS   Homo sapiens.
XX
PN   WO200107611-A2.
XX
PD   01-FEB-2001.
XX
PF   21-JUL-2000; 2000WO-US20006.
XX
PR   26-JUL-1999;   99US-0145701.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Goddard A,  Wood WI;
XX
DR   WPI; 2001-112729/12.
XX
PT   New isolated nucleic acid molecule encoding a SRT polypeptide is useful
PT   for production of recombinant SRT polypeptides, gene mapping,
PT   diagnosing genetic disorders and for gene therapy -
XX
PS   Claim 2; Fig 240; 663pp; English.
XX
CC   Sequences AAF93180 - AAF93743 represent polynucleotide sequences encoding
CC   human SRT proteins. The cDNA sequences are isolated from various
CC   different human tissue cDNA libraries. The invention relates to a method
CC   for detecting cDNA encoding an SRT protein, a vector containing cDNA
CC   encoding SRT, a host cell transformed with the vector, an isolated SRT
CC   polypeptide, and an antibody which binds to SRT. The polynucleotide
CC   sequence can be used in gene therapy and is useful in the recombinant
CC   production of SRT polypeptides, as a hybridisation probe to screen
CC   libraries to isolate cDNAs with sequence identity to SRT polypeptides, to
CC   map the gene encoding the SRT polypeptides and analysing genetic
CC   disorders, tissue typing and disease tissue detection. The SRT
CC   polynucleotide sequences can be used in polymerase chain reaction,
CC   screening for new therapeutic molecules and generation of antisense RNA
CC   and DNA.
XX
```

```
SQ   Sequence 546 BP; 149 A; 129 C; 155 G; 108 T; 5 other;

Alignment Scores:
Pred. No.:              3.02e-32      Length:        546
Score:                  513.50        Matches:       94
Percent Similarity:     55.29%        Conservative:  0
Best Local Similarity:  55.29%        Mismatches:    3
Query Match:            37.56%        Indels:        73
DB:                     22            Gaps:          1

US-10-036-041-2 (1-246) x AAF93419 (1-546)

Qy       1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys 20
           ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db      37 ATGCTTTGGAGGCAGCTCATNTATTGGCAACTGCTGGCTTTGTTTTTCCTCCCTTTTTGC 96

Qy      21 LeuCysGlnAspGluTyrMetGlu---------------------------------- 28
           ||||||||||||||||||||||
Db      97 NTGTGTCAAGATGAATACATGGAGGTGAGCGGAAGAACTAATAAAGTGGTGGCAAGAATA 156

Qy      28 ---------------------------------------------------------- 28

Db     157 GTGCAAAGCCACCAGCAGACTGGCCGTAGCGGCTCCAGGAGGGAGAAAGTGAGAGAGCGG 216

Qy      28 ---------------------------------------------------------- 28

Db     217 AGCCATCCTAAAACTGGGACTGTGGATAATAACACTTNTACAGACCTAAAATCCCTGAGA 276

Qy      28 ---------------------------------------------------------- 28

Db     277 CCAGATGAGCTACCGCACCCCGAGGTAGATGACCTAGCCCAGATCACCACATTCTGGGGC 336

Qy      29 ---SerProGlnThrGlyGlyLeuProProAspCysSerLysCysCysHisGlyAspTyr 47
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     337 CAGTNTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTAC 396

Qy      48 SerPheArgGlyTyrGlnGlyProProGlyProProGlyProProGlyIleProGlyAsn 67
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     397 AGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAAC 456

Qy      68 HisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGluGlyAlaLysGlyGluLysGly 87
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     457 CATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGC 516

Qy      88 AspLysGlyAspLeuGlyProArgGlyGlu 97
           |||||||||||||||||||||||||||||
Db     517 GACAAAGGTGACCTGGGGCCTCGAGGGGAG 546

RESULT 26
ABK35598
ID   ABK35598 standard; DNA; 804 BP.
XX
AC   ABK35598;
XX
DT   08-MAY-2002  (first entry)
XX
DE   Gene encoding novel human secreted or membrane-associated protein #17.
XX
KW   Human; secreted protein; membrane-associated protein; hypertension;
KW   inflammatory disorder; neurological disorder; haematopoietic disorder;
KW   skeletal developmental disorder; growth abnormality; autoimmune disorder;
KW   neurodegenerative disorder; nervous system disorder; bacterial infection;
KW   peripheral myelinopathy; viral infection; cancer; obesity; diabetes;
KW   hypotension; sexual development disorder; blood disorder; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200204600-A2.
XX
PD   17-JAN-2002.
XX
PF   12-JUL-2001; 2001WO-US21985.
XX
PR   12-JUL-2000; 2000US-218033P.
PR   21-AUG-2000; 2000US-226517P.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
PA   (GLAX ) GLAXO GROUP LTD.
XX
PI   Agarwal P,  Cogswell JP,  Lai Y,  Martensen SA,  Rizvi SK,  Strum JC;
PI   Smith RF,  Xiang Z,  Xie Q;
XX
DR   WPI; 2002-188468/24.
DR   P-PSDB; AAU84378.
XX
PT   Novel secreted and membrane-associated polypeptides and polynucleotides
PT   encoding the polypeptides, for preventing, treating and ameliorating
PT   cancers, mental or sexual developmental disorders, and malignant tumours
PT   -
XX
PS   Claim 2; Page 110; 151pp; English.
XX
CC   The present invention relates to the isolation of novel human secreted
CC   or membrane-associated proteins and the genes encoding them. The
CC   sequences of the invention are useful for treating, preventing and
CC   ameliorating various diseases such as inflammatory disorders (e.g.
CC   asthma), neurological disorders (e.g. dementia), haematopoietic
CC   disorders, skeletal developmental disorders, growth abnormalities,
CC   neurodegenerative disorders (e.g. Huntington's disease), nervous system
CC   disorders, autoimmune disorders (e.g. rheumatoid arthritis),
CC   peripheral myelinopathies, viral and bacterial infections,
CC   alpha-mannosidosis, diabetes, cancers, malignant tumours, hyper- and
CC   hypotension, obesity, bulimia, anorexia, manic depression, delirium,
CC   mental retardation, Tourette's syndrome, schizophrenia, growth, mental
CC   or sexual development disorders, and dysfunctions of the blood cascade
CC   system including those leading to stroke. ABK35582-ABK35609 represent
CC   the genes encoding the novel human secreted or membrane-associated
CC   proteins of the invention.
XX
SQ   Sequence 804 BP; 130 A; 293 C; 268 G; 113 T; 0 other;

Alignment Scores:
Pred. No.:              4.37e-17      Length:        804
Score:                  325.00        Matches:       82
Percent Similarity:     48.55%        Conservative:  35
Best Local Similarity:  34.02%        Mismatches:    100
Query Match:            23.77%        Indels:        24
DB:                     24            Gaps:          8

US-10-036-041-2 (1-246) x ABK35598 (1-804)

Qy      21 LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuPro------------ 36
           :::|||                    |||         |||   |||
Db      91 GTGTGCGACCCGCATGGGCCCCGTGGCCCTGGTCCCGACGGCGCGCCTGCTTCCGTGCCC 150

Qy      37 ------ProAspCysSerLysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGly 54
                |||      :::|||         |||              |||   :::|||
Db     151 CCCTTCCCGCCAGGCGCCAAGGGAGAGGTGGGCCGGCGCGGGAAAGCAGGCCTGCGGGGG 210

Qy      55 ProProGlyProProGlyProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsn 74
           ||||||||||||||||||||   |||  ||||||     |||      |||
Db     211 CCCCCTGGACCACCAGGTCCAAGAGGGCCCCCAGGAGAACCCGGCAGGCCAGGCCCCCCG 270

Qy      75 GlyAlaThrGlyHisGluGlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyPro 94
           |||      |||      |||  :::|||      |||      |||      ||||||
Db     271 GGCCCTCCCGGT---CCAGGCCTGCGGGGGCCCCCTGGACCACCAGGTCCAAGAGGGCCC 327

Qy      95 ArgGlyGluArgGlyGlnHisGlyProLysGlyGluLysGlyTyrProGly--------- 111
              ||||||   |||:::   ||||||   |||      |||   ||||||
Db     328 CCAGGAGAACCCGGCAGGCCAGGCCCCCCGGGCCCTCCCGGT---CCAGGTCCGGGCGGG 384

Qy     112 --------------------IleProProGluLeuGlnIleAlaPheMetAlaSerLeu 124
                               :::|||         :::|||||||||   |||   |||
Db     385 GTGGCGCCCGCTGCCGGCTACGTGCCT---------CGCATTGCTTTCTACGCGGGCCTG 435
```

```
Qy    125 AlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerValGluThrAsnIle 144
                                      :::   |||      |||   ||||||:::
Db    436 CGGCGGCCCCACGAGGGTTACGAGGTG---CTGCGCTTCGACGACGTGGTGACCAACGTG 492

Qy    145 GlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSerGlyValTyrPhe 164
          ||||||   ::::::      :::|||:::|||     |||:::   ||||||||||||
Db    493 GGCAACGCCTACGAGGCAGCCAGCGGCAAGTTTACTTGCCCCATGCCAGGCGTCTACTTC 552

Qy    165 PheThrPheSer---MetMetLysHisGluAspValGluGluValTyrValTyrLeuMet 183
          |||   :::      :::|||:::      |||         ::::::      ||||||
Db    553 TTCGCTTACCACGTGCTCATGCGCGGCGGCGACGGCACCAGCATGTGGGCCGACCTCATG 612

Qy    184 HisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLysSerAspThr 203
            ||||||            |||      :::   :::                |||
Db    613 AAGAACGGACAGGTCCGGGCCAGCGCCATTGCTCAGGACGCGGACCAGAACTACGACTAC 672

Qy    204 SerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTrpLeuArgMetGly 223
          :::||||||      :::|||   |||      ||||||||||||:::::::::::::
Db    673 GCCAGCAACAGCGTCATTCTGCACCTGGACGTGGGCGACGAGGTCTTCATCAAGCTGGAC 732

Qy    224 AsnGlyAlaLeuHisGlyAspHis---GlnArgPheSerThrPheAlaGlyPheLeuLeu 242
            |||   :::||||||   :::      ::::::||||||||:::||||||:::::
Db    733 GGCGGGAAAGTGCACGGCGGCAACACCAACAAGTACAGCACCTTCTCCGGCTTCATCATC 792

Qy    243 Phe 243
          :::
Db    793 TAC 795
```

RESULT 27
AAZ61744
ID  AAZ61744 standard; cDNA; 1107 BP.
XX
AC  AAZ61744;
XX
DT  27-MAR-2000  (first entry)
XX
DE  cDNA encoding rat skin cell secreted protein, SEQ ID NO:217.
XX
KW  Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast;
KW  embryonic skin cell; keratinocyte stem cell; transit amplifying cell;
KW  secreted; transmembrane; inflammation; cancer; neurological disease;
KW  angiogenesis; tumour vascularisation; growth disorder;
KW  developmental disorder; skin wound; hair follicle disorder;
KW  anti-inflammatory; cytostatic; neuroprotective; vulnery; ss.
XX
OS  Rattus sp.
XX
PN  WO9955865-A1.
XX
PD  04-NOV-1999.
XX
PF  29-APR-1999;  99WO-NZ00051.
XX
PR  29-APR-1998;  98US-0069726.
PR  09-NOV-1998;  98US-0188930.
XX
PA  (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI  Strachan L,  Sleeman M,  Watson JD,  Onrust R,  Kumble A,  Murison JG;
XX
DR  WPI; 2000-072177/06.
DR  P-PSDB; AAY76039.
XX
PT  Novel polynucleotides useful for the treatment of various conditions
PT  including wounds and cancer -
XX
PS  Claim 1; Page 142-143; 235pp; English.
XX
CC  The invention relates to novel nucleic acid sequences derived from rat
CC  dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,
CC  and mouse embryonic skin, keratinocyte stem cells and transit amplifying
CC  cells. Polypeptides of the invention may be used to treat inflammation,
CC  cancer and neurological diseases. The proteins may be used to stimulate
CC  the growth and motility of keratinocytes, to inhibit the growth of
CC  cancer cells, to modulate angiogenesis and tumour vascularisation, to
CC  modulate skin inflammation, to modulate epithelial cell growth and to
CC  inhibit binding of HIV-1 to leukocytes. The invention may also be used
CC  to treat growth and developmental defects, skin wounds and hair follicle
CC  disorders. Sequences AAZ61606-Z61832 represent cDNA sequences derived
CC  from several mouse, rat or human skin cell types. Sequences
CC  AAZ61606-Z61649, AAZ61725-Z61765, AAZ61802-Z61811 and AAZ61826 encode
CC  proteins with an N-terminal signal sequence, indicating that the proteins
CC  are secreted. Sequences AAZ61650-Z61668, AAZ61766-Z61780, AAZ61812-Z61817
CC  and AAZ61827-Z61829 encode proteins with one or more putative
CC  transmembrane domains.
XX
SQ  Sequence 1107 BP; 273 A; 298 C; 328 G; 208 T; 0 other;

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 3.28e-16 | Length: | 1107 |
| Score: | 316.00 | Matches: | 86 |
| Percent Similarity: | 42.62% | Conservative: | 41 |
| Best Local Similarity: | 28.86% | Mismatches: | 89 |
| Query Match: | 23.12% | Indels: | 82 |
| DB: | 21 | Gaps: | 12 |

US-10-036-041-2 (1-246) x AAZ61744 (1-1107)

```
Qy      6 LeuIleTyrTrpGlnLeuLeuAlaLeuPheLeuProPheCysLeuCysGlnAspGlu 25
          :::|||   |||   |||||||||        ||||||         |||      :::
Db    174 ATGATCTCCTGGATGCTCTTGGCCTGT---GCCCTTCCG---------TGTGCTGCTGAC 221

Qy     26 TyrMet-----------------GluSerProGlnThrGlyGlyLeuProProAspCys 39
            |||                          |||   ||||||       '     |||
Db    222 CCAATGCTTGGTGCCTTTGCTCGCAGGGACTTCCAGAAGGGTGGTCCTCAACTGGTGTGC 281

Qy     40 SerLysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProPro 59
          |||                                    ||||||   |||||||||
Db    282 AGT--------------------------------CTGCCTGGTCCCCAAGGCCCACCT 308

Qy     60 GlyProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHis 79
          ||||||||||||   ||||||::   |||      |||      |||      |||
Db    309 GGCCCTCCAGGAGCACCAGGATCCTCAGGAATGGTGGGAAGAATGGGTTTTCCTGGTAAG 368

Qy     80 GluGlyAlaLysGlyGluLysGlyAspLysGlyAsp------------------------ 91
          :::|||      |||:::   ||||||:::||||||
Db    369 GATGGCCAAGACGGCCAGGACGGAGACCGAGGGGACAGTGGAGAAGAAGGTCCACCTGGC 428

Qy     92 ----------------------------------------------------------Leu 92

Db    429 AGGACAGGCAACCGAGGAAAACAAGGACCAAAGGGCAAAGCTGGGGCCATTGGGAGAGCG 488

Qy     93 GlyProArgGlyGluArg------------------------------------GlyGln 100
          ||||||||||||   :::                                   |||:::
Db    489 GGTCCTCGAGGACCCAAGGGGGTCAGTGGTACCCCCGGGAAACATGGTATACCGGGCAAG 548

Qy    101 HisGlyProLysGlyGluLysGlyTyrProGlyIlePro--------------------- 113
             ||||||||||||:::||||||   ||||||:::|||
Db    549 AAGGGACCTAAGGGCAAGAAAGGGGAACCTGGGCTCCCAGGCCCCTGTAGCTGCGGCAGT 608

Qy    114 ProGluLeuGlnIleAlaPheMetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSer 133
                :::   ||||||      ::::::          :::      :::
Db    609 AGCCGAGCCAAGTCGGCCTTTTCGGTGGCGGTAACCAAGAGTTACCCACGTGAGCGACTG 668

Qy    134 GlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhePheAspValMetThrGly 153
             |||   |||      :::      |||   |||      ::::::      :::|||
Db    669 CCCATCAAGTTTGACAAGATTCTGATGAATGAGGGAGGCCACTACAATGCATCCAGTGGC 728

Qy    154 ArgPheGlyAlaProValSerGlyValTyrPhePheThrPheSerMetMet--------- 170
          :::|||         |||   |||:::|||:::||||||:::   :::
Db    729 AAGTTCGTCTGCAGCGTGCCAGGGATCTATTACTTTACCTATGACATTACGCTGGCCAAC 788

Qy    171 LysHisGluAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsnThrValPhe 190
          ||||||                :::   :::   |||:::||||||||         :::
Db    789 AAACAC--------------CTGGCCATCGGCCTAGTGCACAATGGCCAG------TAC 827
```

```
Qy    191 SerMetTyrSerTyrGluMetLys---GlyLysSerAspThrSerSerAsnHisAlaVal 209
Db    828 CGCATTCGGACTTTTGACGCCAACACCGGCAACCACGACGTGGCCTCGGGCTCCACCATC 887

Qy    210 LeuLysLeuAlaLysGlyAspGluValTrpLeuArgMet-----------GlyAsnGly 225
Db    888 CTAGCTCTCAAGGAGGGTGATGAAGTCTGGTTACAGATTTTCTACTCGGAGCAGAATGGA 947

Qy    226 AlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPheLeuLeuPhe 243
Db    948 CTCTTCTACGACCCTTATTGGACCGACAGCCTGTTCACCGGCTTCCTCATCTAC 1001
```

RESULT 28
AAC99677
ID AAC99677 standard; cDNA; 1107 BP.
XX
AC AAC99677;
XX
DT 08-MAR-2001 (first entry)
XX
DE Skin cell cDNA, SEQ ID NO: 217.
XX
KW Rat; skin cell; cytostatic; antiinflammatory; anti-HIV;
KW nootropic; neuroprotective; vulnerary; immunomodulatory; vaccine;
KW keratinocyte growth stimulation; cancer; angiogenesis inhibition;
KW inflammation; neurological disease; ss.
XX
OS Rattus sp.
XX
PN WO200069884-A2.
XX
PD 23-NOV-2000.
XX
PF 15-MAY-2000; 2000WO-NZ00075.
XX
PR 14-MAY-1999; 99US-0312283.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD, Murison JG;
XX
DR WPI; 2001-007495/01.
DR P-PSDB; AAB55958.
XX
PT New isolated polynucleotide used in the identification of genetic
PT disorders and encoding polypeptides used for treating inflammatory
PT disease, cancer and neurological diseases -
XX
PS Claim 1; Page 186; 352pp; English.
XX
CC The present polynucleotide encodes a polypeptide which is expressed in
CC mammalian skin cells. The polypeptide is useful for stimulating
CC keratinocyte growth and motility, inhibiting the growth of cancer cells,
CC modulating angiogenesis, inhibiting angiogenesis and vascularisation of
CC tumours, modulating skin inflammation, stimulating the growth of
CC epithelial cells, inhibiting the binding of human immunodeficiency virus
CC (HIV)-1 to leukocytes, and treating inflammmatory disease, cancer and
CC neurological diseases. The polynucleotide can be used as a marker, in
CC the identification of genetic disorders, and for the design of
CC oligonucleotides for examining expression patterns.
XX
SQ Sequence 1107 BP; 273 A; 298 C; 328 G; 208 T; 0 other;

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred: No.: | 3.28e-16 | Length: | 1107 |
| Score: | 316.00 | Matches: | 86 |
| Percent Similarity: | 42.62% | Conservative: | 41 |
| Best Local Similarity: | 28.86% | Mismatches: | 89 |
| Query Match: | 23.12% | Indels: | 82 |
| DB: | 22 | Gaps: | 12 |

US-10-036-041-2 (1-246) x AAC99677 (1-1107)

```
Qy      6 LeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCysLeuCysGlnAspGlu 25
Db    174 ATGATCTCCTGGATGCTCTTGGCCTGT---GCCCTTCCG---------TGTGCTGCTGAC 221

Qy     26 TyrMet-----------------GluSerProGlnThrGlyGlyLeuProProAspCys 39
Db    222 CCAATGCTTGGTGCCTTTGCTCGCAGGGACTTCCAGAAGGGTGGTCCTCAACTGGTGTGC 281

Qy     40 SerLysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProPro 59
Db    282 AGT-------------------------------CTGCCTGGTCCCCAAGGCCCACCT 308

Qy     60 GlyProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHis 79
Db    309 GGCCCTCCAGGAGCACCAGGATCCTCAGGAATGGTGGGAAGAATGGGTTTTCCTGGTAAG 368

Qy     80 GluGlyAlaLysGlyGluLysGlyAspLysGlyAsp----------------------- 91
Db    369 GATGGCCAAGACGGCCAGGACGGAGACCGAGGGGACAGTGGAGAAGAAGGTCCACCTGGC 428

Qy     92 ----------------------------------------------------------Leu 92
Db    429 AGGACAGGCAACCGAGGAAAACAAGGACCAAAGGGCAAAGCTGGGGCCATTGGGAGAGCG 488

Qy     93 GlyProArgGlyGluArg-----------------------------------GlyGln 100
Db    489 GGTCCTCGAGGACCCAAGGGGGTCAGTGGTACCCCCGGGAAACATGGTATACCGGGCAAG 548

Qy    101 HisGlyProLysGlyGluLysGlyTyrProGlyIlePro--------------------- 113
Db    549 AAGGGACCTAAGGGCAAGAAAGGGGAACCTGGGCTCCCAGGCCCCTGTAGCTGCGGCAGT 608

Qy    114 ProGluLeuGlnIleAlaPheMetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSer 133
Db    609 AGCCGAGCCAAGTCGGCCTTTTCGGTGGCGGTAACCAAGAGTTACCCACGTGAGCGACTG 668

Qy    134 GlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhePheAspValMetThrGly 153
Db    669 CCCATCAAGTTTGACAAGATTCTGATGAATGAGGGAGGCCACTACAATGCATCCAGTGGC 728

Qy    154 ArgPheGlyAlaProValSerGlyValTyrPhePheThrPheSerMetMet--------- 170
Db    729 AAGTTCGTCTGCAGCGTGCCAGGGATCTATTACTTTACCTATGACATTACGCTGGCCAAC 788

Qy    171 LysHisGluAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsnThrValPhe 190
Db    789 AAACAC--------------CTGGCCATCGGCCTAGTGCACAATGGCCAG------TAC 827

Qy    191 SerMetTyrSerTyrGluMetLys---GlyLysSerAspThrSerSerAsnHisAlaVal 209
Db    828 CGCATTCGGACTTTTGACGCCAACACCGGCAACCACGACGTGGCCTCGGGCTCCACCATC 887

Qy    210 LeuLysLeuAlaLysGlyAspGluValTrpLeuArgMet-----------GlyAsnGly 225
Db    888 CTAGCTCTCAAGGAGGGTGATGAAGTCTGGTTACAGATTTTCTACTCGGAGCAGAATGGA 947

Qy    226 AlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPheLeuLeuPhe 243
Db    948 CTCTTCTACGACCCTTATTGGACCGACAGCCTGTTCACCGGCTTCCTCATCTAC 1001
```

RESULT 29
ABL34829
ID ABL34829 standard; cDNA; 1107 BP.
XX
AC ABL34829; . .
XX
DT 04-APR-2002 (first entry)
XX
DE Rat cDNA isolated from skin cells SEQ ID NO: 217.
XX
KW Human; rat; mouse; skin cell; skin wound; cancer; growth defect;
KW developmental defect; inflammatory disease; dermatological; vulnerary;
KW immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene;

```
KW   ss.
XX
OS   Rattus sp.
XX
PN   WO200190357-A1.
XX
PD   29-NOV-2001.
XX
PF   24-MAY-2001; 2001WO-NZ00099.
XX
PR   24-MAY-2000; 2000US-206650P.
PR   25-JUL-2000; 2000US-221232P.
XX
PA   (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI   Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG, Kumble KD;
XX
DR   WPI; 2002-122020/16.
XX
PT   New polynucleotides and polypeptides encoded by the polynucleotides
PT   isolated from skin cells, useful for treating skin wounds, cancers,
PT   growth and developmental defects, inflammatory diseases, or for
PT   modulating immune responses
XX
PS   Claim 1; Page 161; 466pp; English.
XX
CC   The present invention provides the protein and coding sequences of cDNAs
CC   isolated from human, murine and rat skin cell libraries. The sequences
CC   can be used in the development of therapeutic agents useful in the
CC   treatment of skin diseases, including skin wounds, cancer, growth
CC   defects, developmental defects and inflammatory diseases. The proteins
CC   have important roles in the induction of hair growth, cell proliferation
CC   and cell-cell interaction, in maintaining tissue integrity, in wound
CC   healing and in modulating immune responses. The present sequence is a
CC   cDNA of the invention.
XX
SQ   Sequence 1107 BP; 273 A; 298 C; 328 G; 208 T; 0 other;

Alignment Scores:
Pred. No.:                3.28e-16        Length:         1107
Score:                    316.00          Matches:        86
Percent Similarity:       42.62%          Conservative:   41
Best Local Similarity:    28.86%          Mismatches:     89
Query Match:              23.12%          Indels:         82
DB:                       24              Gaps:           12

US-10-036-041-2 (1-246) x ABL34829 (1-1107)

Qy       6 LeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCysLeuCysGlnAspGlu 25
Db     174 ATGATCTCCTGGATGCTCTTGGCCTGT---GCCCTTCCG---------TGTGCTGCTGAC 221

Qy      26 TyrMet-----------------GluSerProGlnThrGlyGlyLeuProProAspCys 39
Db     222 CCAATGCTTGGTGCCTTTGCTCGCAGGGACTTCCAGAAGGGTGGTCCTCAACTGGTGTGC 281

Qy      40 SerLysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProPro 59
Db     282 AGT-------------------------------CTGCCTGGTCCCCAAGGCCCACCT 308

Qy      60 GlyProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHis 79
Db     309 GGCCCTCCAGGAGCACCAGGATCCTCAGGAATGGTGGGAAGAATGGGTTTTCCTGGTAAG 368

Qy      80 GluGlyAlaLysGlyGluLysGlyAspLysGlyAsp---------------------- 91
Db     369 GATGGCCAAGACGGCCAGGACGGAGACCGAGGGGACAGTGGAGAAGAAGGTCCACCTGGC 428

Qy      92 ----------------------------------------------------------Leu 92

Db     429 AGGACAGGCAACCGAGGAAAACAAGGACCAAAGGGCAAAGCTGGGGCCATTGGGAGAGCG 488

Qy      93 GlyProArgGlyGluArg-----------------------------------GlyGln 100
Db     489 GGTCCTCGAGGACCCAAGGGGGTCAGTGGTACCCCCGGGAAACATGGTATACCGGGCAAG 548

Qy     101 HisGlyProLysGlyGluLysGlyTyrProGlyIlePro---------------------- 113
Db     549 AAGGGACCTAAGGGCAAGAAAGGGGAACCTGGGCTCCCAGGCCCCTGTAGCTGCGGCAGT 608

Qy     114 ProGluLeuGlnIleAlaPheMetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSer 133
Db     609 AGCCGAGCCAAGTCGGCCTTTTCGGTGGCGGTAACCAAGAGTTACCCACGTGAGCGACTG 668

Qy     134 GlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhePheAspValMetThrGly 153
Db     669 CCCATCAAGTTTGACAAGATTCTGATGAATGAGGGAGGCCACTACAATGCATCCAGTGGC 728

Qy     154 ArgPheGlyAlaProValSerGlyValTyrPhePheThrPheSerMetMet--------- 170
Db     729 AAGTTCGTCTGCAGCGTGCCAGGGATCTATTACTTTACCTATGACATTACGCTGGCCAAC 788

Qy     171 LysHisGluAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsnThrValPhe 190
Db     789 AAACAC--------------CTGGCCATCGGCCTAGTGCACAATGGCCAG------TAC 827

Qy     191 SerMetTyrSerTyrGluMetLys---GlyLysSerAspThrSerSerAsnHisAlaVal 209
Db     828 CGCATTCGGACTTTTGACGCCAACACCGGCAACCACGACGTGGCCTCGGGCTCCACCATC 887

Qy     210 LeuLysLeuAlaLysGlyAspGluValTrpLeuArgMet-----------GlyAsnGly 225
Db     888 CTAGCTCTCAAGGAGGGTGATGAAGTCTGGTTACAGATTTTCTACTCGGAGCAGAATGGA 947

Qy     226 AlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPheLeuLeuPhe 243
Db     948 CTCTTCTACGACCCTTATTGGACCGACAGCCTGTTCACCGGCTTCCTCATCTAC 1001

RESULT 30
AAD16350
ID   AAD16350 standard; DNA; 870 BP.
XX
AC   AAD16350;
XX
DT   19-NOV-2001  (first entry)
XX
DE   Human SBhACRP30a gene #1.
XX
KW   Human; Alzheimer's disease; amyotrophic lateral sclerosis;
KW   ALS; Zollinger-Ellison syndrome; immune system disease; schizophrenia;
KW   inflammation; haematopoietic disease; anxiety; feeding disorder; aging;
KW   anorexia; depression; cardiovascular disease; sleep disorder; seizure;
KW   memory alteration; migraine; stroke; asthma; neuropathy; hypoglycaemia;
KW   sexual disorder; growth abnormality; infection; autoimmune disease;
KW   rheumatoid arthritis; cataractogenesis; angiogenesis; atherosclerosis;
KW   cerebral ischaemia; cirrhosis; Huntington's disease; Hodgson's disease;
KW   hypercholesterolaemia; headache; amnesia; cardiac arrhythmia; obesity;
KW   diabetes mellitus; glomerulonephritis; renovascular hypertension;
KW   cancer; vaccine; gene therapy; SBhACRP30a gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..870
FT                   /*tag= a
FT                   /product= "Human SBhACRP30a protein #1"
FT                   /transl_except= (pos:235..243, aa:Ala-Leu)
XX
PN   WO200160850-A1.
XX
PD   23-AUG-2001.
XX
PF   14-FEB-2001; 2001WO-US04703.
XX
PR   14-FEB-2000; 2000US-0182172.
PR   29-FEB-2000; 2000US-0186084.
```

PR 18-APR-2000; 2000US-0198583.
PR 04-OCT-2000; 2000US-0237963.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Agarwal P, Kabnick KS, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;
XX
DR WPI; 2001-536566/59.
DR P-PSDB; AAE09443.
XX
PT New secreted and membrane associated polypeptides for treating
PT Alzheimer's disease, psoriasis, cancer, enterocolitis, sleep and sexual
PT disorders, stroke, and asthma
XX
PS Claim 2; Page 41; 94pp; English.
XX
CC The present sequence is a gene encoding human SBhACRP30a protein,
CC a secreted protein of the invention.
CC The invention relates to secreted and membrane associated polypeptides
CC and nucleic acid molecules encoding such polypeptides. Sequences of the
CC invention are useful for treating diseases such as Alzheimer's disease,
CC amyotrophic lateral sclerosis (ALS), Zollinger-Ellison syndrome, diseases
CC of the immune system, haematopoietic disease, inflammation, anxiety,
CC schizophrenia, feeding disorders, anorexia, depression, social, sexual
CC and rewarded behaviour, cardiovascular disease, sleep disorder, learning
CC and memory alteration and altered immune response, seizure, migraine,
CC cancer, stroke, asthma, neuropathy, aging, sexual disorders, treatment
CC of transsexuals, growth abnormalities, obesity, infections, autoimmune
CC diseases (e.g. rheumatoid arthritis), cataractogenesis, angiogenesis,
CC disorders associated with healthy maintenance of gastric mucosa and
CC repair of acute and chronic mucosal lesion, lung carcinoma, cerebral
CC ischaemia, atherosclerosis, cirrhosis, Huntington's disease, headache,
CC amnesia, multiple sclerosis, Hodgson's disease, dilated cardiomyopathy,
CC congestive heart failure, cardiac arrhythmias, hypercholesterolaemia,
CC viral and non-viral hepatitis, type I and type II diabetes mellitus,
CC glomerulonephritis, renovascular hypertension, hypoglycaemia, periodic
CC paralyses, tendinitis and malignant hyperthermia. Polypeptides of the
CC invention are used to identify membrane bound and soluble receptors.
CC They are also useful as vaccines for inducing an immunological response
CC in a mammal. Polynucleotides of the invention are used in gene therapy.
CC They are also valuable for chromosome localisation studies and tissue
CC expression studies.
XX
SQ Sequence 870 BP; 239 A; 200 C; 237 G; 194 T; 0 other;

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 2.98e-16 | Length: | 870 |
| Score: | 315.00 | Matches: | 86 |
| Percent Similarity: | 41.26% | Conservative: | 32 |
| Best Local Similarity: | 30.07% | Mismatches: | 96 |
| Query Match: | 23.04% | Indels: | 72 |
| DB: | 22 | Gaps: | 9 |

US-10-036-041-2 (1-246) x AAD16350 (1-870)

```
Qy     14 LeuPhePheLeuProPheCysLeuCysGlnAspGluTyrMetGluSerProGlnThrGly 33
          |||::: |||  :::|||                    |||
Db     13 CTCTATGTTACAAGTTTTGCCATTTGTGCCAGTGGACAACCCCGGGGTAATCAGTTGAAA 72

Qy     34 GlyLeuProProAspCysSerLysCysCysHisGlyAspTyrSerPheArgGlyTyrGln 53
          |||                 |||          |||     |||
Db     73 GGAGAGAACTACTCCCCCAGGTATATCTGC----------AGCATTCCTGGCTTGCCT 120

Qy     54 GlyProProGlyProProGlyProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsn 73
          ||||||||||||||||||||      |||  ||||||  ||||||     |||
Db    121 GGACCTCCAGGGCCCCCTGGAGCAAATGGTTCCCCTGGGCCCCATGGTCGCATCGGCCTT 180

Qy     74 AsnGlyAlaThrGlyHisGluGlyAlaLysGlyGluLysGlyAsp--------------- 88
             |||      |||  :::|||  ||||||||||||||:::
Db    181 CCAGGAAGAGATGGTAGAGACGGCAGGAAAGGAGAGAAAGGTGAAAAGGGAACTGCAGGT 240

Qy     88 ------------------------------------------------------------ 88
```

```
Db    241 TTGAGAGGTAAGACTGGACCGCTAGGTCTTGCCGGTGAGAAAGGGGACCAAGGAGAGACT 300

Qy     89 ------LysGlyAspLeuGlyProArgGlyGluArgGlyGlnHisGlyPro--------- 103
              ||||||  :::||||||  ||||||:::|||:::  ||||||
Db    301 GGGAAGAAAGGACCCATAGGACCAGAGGGAGAGAAAGGAGAAGTAGGTCCAATTGGTCCT 360

Qy    104 ------------------LysGlyGluLysGlyTyrProGlyIleProPro--------- 114
                           :::||||||:::|||  ||||||:::|||
Db    361 CCTGGACCAAAGGGAGACAGAGGAGAACAAGGGGACCCGGGGCTGCCTGGAGTTTGCAGA 420

Qy    115 -----------GluLeuGlnIleAlaPheMetAlaSerLeuAlaThrHisPheSerAsn 130
                      |||:::  ||||||        :::  |||  :::
Db    421 TGTGGAAGCATCGTGCTCAAATCCGCCTTTTCTGTTGGCATCACAACCAGCTACCCAGAA 480

Qy    131 GlnAsnSerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhePheAspVal 150
          :::  ||||||||:::  |||      |||  |||      ::::::
Db    481 GAAAGACTACCTATTATATTTAACAAGGTCCTCTTCAACGAGGGAGAGCACTACAACCCT 540

Qy    151 MetThrGlyArgPheGlyAlaProValSerGlyValTyrPhePheThrPheSerMetMet 170
          ||||||:::|||              |||:::|||:::|||::::::  :::
Db    541 GCCACAGGGAAGTTCATCTGTGCTTTCCCAGGGATCTATTACTTTTCTTATGATATCACA 600

Qy    171 ---------LysHisGluAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsn 187
                 ||||||              :::  :::  |||:::||||||||
Db    601 TTGGCTAATAAGCAT--------------CTGGCAATCGGACTGGTACACAATGGG--- 642

Qy    188 ThrValPheSerMetTyrSerTyrGluMetLys-----------------GlyLysSer 201
                              |||  :::|||                 |||
Db    643 ------------------CAATACCGGATAAAGACCTTCGACGCCAACACAGGAAACCAT 684

Qy    202 AspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTrpLeuArg 221
          |||  :::|||         |||:::  |||         ||||||||||||||||
Db    685 GATGTGGCTTCGGGGTCCACAGTCATCTATCTGCAGCCAGAAGATGAAGTCTGGCTGGAG 744

Qy    222 Met------------GlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPhe 237
          :::              ||||||                          |||  |||
Db    745 ATTTTCTTCACAGACCAGAATGGCCTCTTCTCAGACCCAGGTTGGGCAGACAGCTTATTC 804

Qy    238 AlaGlyPheLeuLeuPhe 243
          :::|||||||||||||:::
Db    805 TCCGGGTTTCTCTTATAC 822
```

Search completed: March 13, 2003, 18:19:54
Job time : 280 secs

```
CC   The present sequence is one of a large number of 5' ESTs derived from
CC   mRNAs encoding secreted proteins. An ORF has been identified within the
CC   sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
CC   derived from 30 different tissues. EST sequences usually correspond
CC   mainly to the 3' untranslated region (UTR) of the mRNA because they are
CC   often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
CC   well suited for isolating cDNA sequences derived from the 5' ends of
CC   mRNAs and even in those cases where longer cDNA sequences have been
CC   obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
CC   mRNAs with intact 5' ends and can therefore be used to obtain full length
CC   cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
CC   gene therapy and chromosome mapping procedures. They are used to obtain
CC   upstream regulatory sequences and to design expression and secretion
CC   vectors.
XX
SQ   Sequence 471 BP; 107 A; 130 C; 134 G; 99 T; 1 other;

  Query Match             26.4%;  Score 452;  DB 21;  Length 471;
  Best Local Similarity   99.6%;  Pred. No. 4.4e-121;
  Matches  452;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GGCATCTGCCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGA 60
Db      12 GGCATCTGCCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGA 71

Qy      61 GGCTCTGTTGAGAATCATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTT 120
Db      72 GGCTCTGTTGAGAATCATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTT 131

Qy     121 TTTCCTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACT 180
Db     132 TTTCCTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACT 191

Qy     181 ACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCC 240
Db     192 ACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCC 251

Qy     241 CCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGG 300
Db     252 CCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGG 311

Qy     301 AGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCG 360
Db     312 AGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCG 371

Qy     361 AGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGA 420
Db     372 AGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGA 431

Qy     421 ACTTCAGATTGCATTCATGGCTTCTCTGGCAACC 454
Db     432 ACTTCAGATTGCATTCATGGCTTCTCTGGMACCC 465


DT 25
9551
AAX39551 standard; DNA; 472 BP.

AAX39551;

21-JUN-1999  (first entry)

Human secreted protein 5' EST SEQ ID No 149.

Human; secreted protein; EST; expressed sequence tag; diagnosis;
forensic; gene therapy; chromosome mapping; signal peptide;
upstream regulatory sequence; cytokine activity; cell proliferation;
differentiation; haematopoiesis regulation; tissue growth regulation;
reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
thrombolytic; anti-inflammatory; tumour inhibition; ds.

Homo sapiens.

PN   WO9906551-A2.
XX
PD   11-FEB-1999.
XX
PF   31-JUL-1998;   98WO-IB01235.
XX
PR   01-AUG-1997;   97US-0905133.
XX
PA   (GEST ) GENSET.
XX
PI   Duclert A,  Dumas Milne Edwards J,  Lacroix B;
XX
DR   WPI; 1999-153781/13.
DR   P-PSDB; AAY11485.
XX
PT   New nucleic acids encoding human secreted - proteins obtained from
PT   cDNA libraries prepared from substantia nigra, cerebellum, surrenals
PT   and fetal brain tissue
XX
PS   Claim 1; Page 263; 434pp; English.
XX
CC   AAX39440 to AAX39597 represent 5' expressed sequence tags (ESTs) for
CC   human secreted proteins, and encode the proteins given in AAY11374 to
CC   AAY11531, respectively. The proteins given represent the signal peptide
CC   and an N-terminal fragment of a secreted protein. The nucleic acid
CC   sequences can be used for producing secreted human gene products. They
CC   can also be used to develop products for diagnosis and therapy. The
CC   proteins obtained may have cytokine activity, cell
CC   proliferation/differentiation activity, haematopoiesis regulating
CC   activity, tissue growth regulating activity, reproductive hormone
CC   regulating activity, chemotactic/ chemokinetic activity, haemostatic and
CC   thrombolytic activity, receptor/ ligand activity, anti-inflammatory
CC   activity, tumour inhibition activity or other activities. The products
CC   can be used in forensic, gene therapy and chromosome mapping procedures.
CC   The sequences can also be used for obtaining corresponding promoter
CC   sequences. The nucleic acids encoding the signal peptide can be used for
CC   directing extracellular secretion of a polypeptide or the insertion of a
CC   polypeptide into a membrane, or importing a polypeptide into a cell.
XX
SQ   Sequence 472 BP; 108 A; 130 C; 134 G; 99 T; 1 other;

  Query Match             26.4%;  Score 452;  DB 20;  Length 472;
  Best Local Similarity   99.6%;  Pred. No. 4.4e-121;
  Matches  452;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GGCATCTGCCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGA 60
Db      13 GGCATCTGCCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGA 72

Qy      61 GGCTCTGTTGAGAATCATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTT 120
Db      73 GGCTCTGTTGAGAATCATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTT 132

Qy     121 TTTCCTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACT 180
Db     133 TTTCCTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACT 192

Qy     181 ACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCC 240
Db     193 ACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCC 252

Qy     241 CCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGG 300
Db     253 CCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGG 312

Qy     301 AGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCG 360
Db     313 AGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCG 372

Qy     361 AGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGA 420
Db     373 AGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGA 432
```

```
Qy    421 ACTTCAGATTGCATTCATGGCTTCTCTGGCAACC 454
          ||||||||||||||||||||||||||||||:|| ||
Db    433 ACTTCAGATTGCATTCATGGCTTCTCTGGMACCC 466
```

RESULT 26
ABV56781
ID  ABV56781 standard; cDNA; 472 BP.
XX
AC  ABV56781;
XX
DT  17-SEP-2002  (first entry)
XX
DE  Human prostate expression marker cDNA 56772.
XX
KW  Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW  pharmacogenomic marker; gene; ss.
XX
OS  Homo sapiens.
XX
PN  WO200160860-A2.
XX
PD  23-AUG-2001.
XX
PF  20-FEB-2001; 2001WO-US05171.
XX
PR  17-FEB-2000; 2000US-183319P.
PR  16-MAR-2000; 2000US-189862P.
PR  25-MAY-2000; 2000US-207454P.
PR  09-JUN-2000; 2000US-211314P.
PR  18-JUL-2000; 2000US-219007P.
PR  13-DEC-2000; 2000US-255281P.
XX
PA  (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI  Schlegel R,  Endege WO,  Monahan JE;
XX
DR  WPI; 2001-662795/76.
XX
PT  Novel isolated nucleic acid molecule associated with cancerous state of
PT  prostate cells and correlating with presence of prostate cancer, useful
PT  for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS  Claim 1; Page 10943; 11750pp; English.
XX
CC  The invention relates to an isolated nucleic acid molecule (I) comprising
CC  a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC  specification or its complement. (I) is useful for:
CC  (a) assessing whether a patient is afflicted with prostate cancer;
CC  (b) monitoring the progression of prostate cancer in a patient;
CC  (c) assessing the efficacy of a test compound to inhibit prostate
CC  cancer in a patient;
CC  (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC  in a patient;
CC  (e) selecting a composition for inhibiting prostate cancer in a patient;
CC  (f) assessing the prostate cell carcinogenic potential of a compound;
CC  (g) determining whether prostate cancer has metastasized in a patient;
CC  (h) assessing the aggressiveness or indolence of prostate cancer in a
CC  patient;
CC  (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
XX
SQ  Sequence 472 BP; 141 A; 105 C; 92 G; 134 T; 0 other;

  Query Match             20.2%;  Score 345.6;  DB 23;  Length 472;
  Best Local Similarity   87.7%;  Pred. No. 4.4e-90;
  Matches  400;  Conservative    0;  Mismatches   54;  Indels    2;  Gaps    2;

```
Qy    587 AAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATGG-CAACACAGT-CT 644
          || ||||||||||| |||||||||| ||||| |||||||||||||||| ||||||||| ||
Db     17 AACCATGAGGATGTGGAGGAAGTGTTTGTGTTCCTTATGCACAATGGCCAACACAGTCCT 76

Qy    645 TCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCAATCATGCTGTGC 704
          ||||||||| ||| ||| ||| |||||||||||||| || | |||| || || | ||||||
Db     77 TCAGCATGTCCAGTTATAAAAGGAAGGGCAAATCAAATCCTTCCACCATTCTTCCTGTGC 136

Qy    705 TGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTCCATGGGG 764
          | || ||| |||||||||| ||||| | |||| |||||||||||||| || || ||||||
Db    137 TAAACCTACCCAAAGGGGATAAGGTTGGCCTGCAAATGGGCAATGGCTCTTTCTATGGGG 196

Qy    765 ACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTAAGTAAATATATG 824
          |||||||||||||||||| ||||||||| |||||| |||||| |||| ||||||| ||
Db    197 ACCACCAACGCTTCTCCACTTTTGCAGGATCCCTGCTTTTTGAACCTAATTAAATATTTG 256

Qy    825 ACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCTGATTTGTTACGATCTGAGG 884
          |||| |||  ||||| |||||| || ||||||| |||| |||||||||| | ||||||||
Db    257 ACTAAAATCCCTCCATTTTGGGAAAAACTTGTACCTGACCTGATTTGTTCCAATCTGAGG 316

Qy    885 AACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATTATTGGTTGCAATGTTGT 944
          |||||||||| |||||||||| ||||||||  |||||||||| ||||||||||||||||
Db    317 AACATTAAAGTGGAGGGTTTTACTTTGCTGTATAAAAAAAATTATGGGTTGCAATGTTGT 376

Qy    945 TCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGAAGAATCAACCACA 1004
          |||| ||||||| ||||||||||||||||||||||||||||||||| || | ||| |||||
Db    377 TCACCCTACAGGCACACCAATAATGTTGGACAATTCAGGGGCTCAAAAAACTCACCCACA 436

Qy   1005 AAATAGTCTTCTCAGATGACCTTGACTAATATACTC 1040
          ||||||| |||||| ||||||||||||||||||||
Db    437 AAATAGTTTTCTCAAATGACCTTGACTAATATACTC 472
```

RESULT 27
AAF93419
ID  AAF93419 standard; cDNA; 546 BP.
XX
AC  AAF93419;
XX
DT  21-MAY-2001  (first entry)
XX
DE  cDNA encoding SRT protein isolated from prostate tissue SEQ ID 240.
XX
KW  Human; SRT; gene therapy; gene mapping; tissue typing; ss.
XX
OS  Homo sapiens.
XX
PN  WO200107611-A2.
XX
PD  01-FEB-2001.
XX
PF  21-JUL-2000; 2000WO-US20006.
XX
PR  26-JUL-1999;  99US-0145701.
XX
PA  (GETH ) GENENTECH INC.
XX
PI  Baker KP,  Goddard A,  Wood WI;
XX
DR  WPI; 2001-112729/12.
XX
PT  New isolated nucleic acid molecule encoding a SRT polypeptide is useful
PT  for production of recombinant SRT polypeptides, gene mapping,
PT  diagnosing genetic disorders and for gene therapy -
XX
PS  Claim 2; Fig 240; 663pp; English.
XX
CC  Sequences AAF93180 - AAF93743 represent polynucleotide sequences encoding
CC  human SRT proteins. The cDNA sequences are isolated from various
CC  different human tissue cDNA libraries. The invention relates to a method
CC  for detecting cDNA encoding an SRT protein, a vector containing cDNA
CC  encoding SRT, a host cell transformed with the vector, an isolated SRT
CC  polypeptide, and an antibody which binds to SRT. The polynucleotide
CC  sequence can be used in gene therapy and is useful in the recombinant
CC  production of SRT polypeptides, as a hybridisation probe to screen
CC  libraries to isolate cDNAs with sequence identity to SRT polypeptides, to
CC  map the gene encoding the SRT polypeptides and analysing genetic
CC  disorders, tissue typing and disease tissue detection. The SRT
CC  polynucleotide sequences can be used in polymerase chain reaction,

```
AAX39551
ID   AAX39551 standard; DNA; 472 BP.
XX
AC   AAX39551;
XX
DT   21-JUN-1999  (first entry)
XX
DE   Human secreted protein 5' EST SEQ ID No 149.
XX
KW   Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW   forensic; gene therapy; chromosome mapping; signal peptide;
KW   upstream regulatory sequence; cytokine activity; cell proliferation;
KW   differentiation; haematopoiesis regulation; tissue growth regulation;
KW   reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW   thrombolytic; anti-inflammatory; tumour inhibition; ds.
XX
OS   Homo sapiens.
XX
PN   WO9906551-A2.
XX
PD   11-FEB-1999.
XX
PF   31-JUL-1998;   98WO-IB01235.
XX
PR   01-AUG-1997;   97US-0905133.
XX
PA   (GEST ) GENSET.
XX
PI   Duclert A, Dumas Milne Edwards J, Lacroix B;
XX
DR   WPI; 1999-153781/13.
DR   P-PSDB; AAY11485.
XX
PT   New nucleic acids encoding human secreted - proteins obtained from
PT   cDNA libraries prepared from substantia nigra, cerebellum, surrenals
PT   and fetal brain tissue
XX
PS   Claim 1; Page 263; 434pp; English.
XX
CC   AAX39440 to AAX39597 represent 5' expressed sequence tags (ESTs) for
CC   human secreted proteins, and encode the proteins given in AAY11374 to
CC   AAY11531, respectively. The proteins given represent the signal peptide
CC   and an N-terminal fragment of a secreted protein. The nucleic acid
CC   sequences can be used for producing secreted human gene products. They
CC   can also be used to develop products for diagnosis and therapy. The
CC   proteins obtained may have cytokine activity, cell
CC   proliferation/differentiation activity, haematopoiesis regulating
CC   activity, tissue growth regulating activity, reproductive hormone
CC   regulating activity, chemotactic/ chemokinetic activity, haemostatic and
CC   thrombolytic activity, receptor/ ligand activity, anti-inflammatory
CC   activity, tumour inhibition activity or other activities. The products
CC   can be used in forensic, gene therapy and chromosome mapping procedures.
CC   The sequences can also be used for obtaining corresponding promoter
CC   sequences. The nucleic acids encoding the signal peptide can be used for
CC   directing extracellular secretion of a polypeptide or the insertion of a
CC   polypeptide into a membrane, or importing a polypeptide into a cell.
XX
SQ   Sequence 472 BP; 108 A; 130 C; 134 G; 99 T; 1 other;

Alignment Scores:
Pred. No.:                8.58e-49        Length:         472
Score:                    721.00          Matches:        127
Percent Similarity:       99.22%          Conservative:   0
Best Local Similarity:    99.22%          Mismatches:     1
Query Match:              52.74%          Indels:         1
DB:                       20              Gaps:           0

US-10-036-041-2 (1-246) x AAX39551 (1-472)

Qy       1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      89 ATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTCCTCCCTTTTTGC 148

Qy      21 LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     149 CTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGT 208

Qy      41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     209 AAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGC 268

Qy      61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     269 CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAA 328

Qy      81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     329 GGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAG 388

Qy     101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     389 CATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTC 448

Qy     121 MetAlaSerLeuAlaThrHisPhe 128
           |||||||||||  |||||||||
Db     449 ATGGCTTCTCTGGM-ACCCACTTC 471

RESULT 25
AAF93419
ID   AAF93419 standard; cDNA; 546 BP.
XX
AC   AAF93419;
XX
DT   21-MAY-2001  (first entry)
XX
DE   cDNA encoding SRT protein isolated from prostate tissue SEQ ID 240.
XX
KW   Human; SRT; gene therapy; gene mapping; tissue typing; ss.
XX
OS   Homo sapiens.
XX
PN   WO200107611-A2.
XX
PD   01-FEB-2001.
XX
PF   21-JUL-2000; 2000WO-US20006.
XX
PR   26-JUL-1999;   99US-0145701.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Goddard A,  Wood WI;
XX
DR   WPI; 2001-112729/12.
XX
PT   New isolated nucleic acid molecule encoding a SRT polypeptide is useful
PT   for production of recombinant SRT polypeptides, gene mapping,
PT   diagnosing genetic disorders and for gene therapy -
XX
PS   Claim 2; Fig 240; 663pp; English.
XX
CC   Sequences AAF93180 - AAF93743 represent polynucleotide sequences encoding
CC   human SRT proteins. The cDNA sequences are isolated from various
CC   different human tissue cDNA libraries. The invention relates to a method
CC   for detecting cDNA encoding an SRT protein, a vector containing cDNA
CC   encoding SRT, a host cell transformed with the vector, an isolated SRT
CC   polypeptide, and an antibody which binds to SRT. The polynucleotide
CC   sequence can be used in gene therapy and is useful in the recombinant
CC   production of SRT polypeptides, as a hybridisation probe to screen
CC   libraries to isolate cDNAs with sequence identity to SRT polypeptides, to
CC   map the gene encoding the SRT polypeptides and analysing genetic
CC   disorders, tissue typing and disease tissue detection. The SRT
CC   polynucleotide sequences can be used in polymerase chain reaction,
CC   screening for new therapeutic molecules and generation of antisense RNA
CC   and DNA.
XX
```